



# STIC Search Report

## Biotech-Chem Library

STIC Database Tracking Number: 160995

TO: Ruixiang Li  
Location: REM/4D75/4C70  
Art Unit: 1646  
Monday, August 08, 2005

Case Serial Number: 10/626126

From: Edward Hart  
Location: Biotech-Chem Library  
REM-1A55  
Phone: 571-272-2512

[edward.hart@uspto.gov](mailto:edward.hart@uspto.gov)

### Search Notes

Examiner Li,

Here are the results of the search you requested.

Please feel free to contact me if you have any questions.

Edward Hart

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**~~BEST AVAILABLE COPY~~**

STIC-Biotech/ChemLib

168995

From: Li, Ruixiang  
Sent: Friday, July 29, 2005 4:06 PM  
To: STIC-Biotech/ChemLib  
Subject: Sequence search of Application No.10/626,126

Please do a standard search on:

- (i). SEQ ID NO: 9 against commercial amino acid databases.
- (ii). SEQ ID NOS: 6 and 9 against commercial nucleic acid databases.

Thank you very much!

Ruixiang Li  
GAU 1646  
REM 4D75  
Mail Box 4C70  
(571) 272-0875

RECEIVED  
JUL 29 2005  
STIC-Biotech Division  
(STIC)

\*\*\*\*\*

STAFF USE ONLY

Searcher: \_\_\_\_\_  
Searcher Phone: 2- \_\_\_\_\_  
Date Searcher Picked up: 8/1/05  
Date Completed: \_\_\_\_\_  
Searcher Prep/Rev. Time: \_\_\_\_\_  
Online Time: \_\_\_\_\_

\*\*\*\*\*

Type of Search

NA#: 1 AA#: 171 reverse to NA  
Interference: \_\_\_\_\_ SPDI: \_\_\_\_\_  
S/L: \_\_\_\_\_ Oligomer: \_\_\_\_\_  
Encode/Transl: \_\_\_\_\_  
Structure#: \_\_\_\_\_ Text: \_\_\_\_\_  
Inventor: \_\_\_\_\_ Litigation: \_\_\_\_\_

\*\*\*\*\*

Vendors and cost where applicable

STN: \_\_\_\_\_  
DIALOG: \_\_\_\_\_  
QUESTEL/ORBIT: \_\_\_\_\_  
LEXIS/NEXIS: \_\_\_\_\_  
SEQUENCE SYSTEM: OSp  
WWW/Internet: \_\_\_\_\_  
Other(Specify): \_\_\_\_\_

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QY 61 TTAATGTCCTGCTGCTTTGCTATAAACGATAGGCAATGCTGTGGTCAATTTTAGCCCTTT 120
Db 61 TTAATGTCCTGCTGCTTTGCTATAAACGATAGGCAATGCTGTGGTCAATTTTAGCCCTTT 120

QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTAATTTTCTTAATTTGGCTATTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTAATTTTCTTAATTTGGCTATTCT 180

QY 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG 240

QY 241 AATTTTGGAGTGGAAATCTGCAATGTTTTGGCTCAATTAAGTCAATCTTTTGTGCACAGCA 300
Db 241 AATTTTGGAGTGGAAATCTGCAATGTTTTGGCTCAATTAAGTCAATCTTTTGTGCACAGCA 300

QY 301 TCCGCTCTACAGTATTGTCCTCATTTAGCTAGCATCGATACGATCAGTTCAGTTCCTGCTGTG 360
Db 301 TCCGCTCTACAGTATTGTCCTCATTTAGCTAGCATCGATACGATCAGTTCAGTTCCTGCTGTG 360

QY 361 CGTTATAGACACAGACACTGGCATCTGGAATTTGCTCAAAATGTTGCTCAAAATGTTGTTGG 420
Db 361 CGTTATAGACACAGACACTGGCATCTGGAATTTGCTCAAAATGTTGCTCAAAATGTTGTTGG 420

QY 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480

QY 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTACA 540
Db 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTACA 540

QY 541 GCATTTCTGGAAATTCCTGCTCCCTGTCTCTGGTGGTCTATTTTCAAGTACAGATTAC 600
Db 541 GCATTTCTGGAAATTCCTGCTCCCTGTCTCTGGTGGTCTATTTTCAAGTACAGATTAC 600

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Db 601 TGGAGCTGTGGAGCGTGGAGTCTCAGTAGGTGGCTAGCCCTAGCCAGCTGGATTCATCGCT 660

QY 661 ACCTCTTCCAGGGCACTGGACACTCAGCAGAACTGGGTTGGCTGTAGACAAAGTCTT 720
Db 661 ACCTCTTCCAGGGCACTGGACACTCAGCAGAACTGGGTTGGCTGTAGACAAAGTCTT 720

QY 721 CTTGGATTAAGGAAACAGCGCGATCCCTTCATTCAGAAAGTCCACAGGAAAGAGCAGT 780
Db 721 CTTGGATTAAGGAAACAGCGCGATCCCTTCATTCAGAAAGTCCACAGGAAAGAGCAGT 780

QY 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGTTCC 840
Db 781 CTCTGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAGTGGTTCC 840

QY 841 TTCTGCGATCAGAAAGCCAGTCTTCCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCGATCAGAAAGCCAGTCTTCCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900

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QY 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020

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Db 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACCTTATTAATTCCTTCTATAC 1080

QY 1081 CCTTTGGCCACAGACGTTTCCAGAAAGCTTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGGCCACAGACGTTTCCAGAAAGCTTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
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QY 1141 CCAGCACCTTTCAGAGCCAGTCCAGTATCTTCTTGA 1176
Db 1141 CCAGCACCTTTCAGAGCCAGTCCAGTATCTTCTTGA 1176

RESULT 2
US-10-626-126-6
; Sequence 6, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patentin version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
US-10-626-126-6

Query Match 100.0%; Score 1176; DB 21; Length 1176;
Best Local Similarity 100.0%; Pred. No. 0;
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1 ATGTCGGAGTCTAACGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGTCGGAGTCTAACGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60

QY 61 TTAATGTCCTGCTGCTTTTGTATAACGATAGGCAATGCTGTGGTCAATTTTAGCCCTTT 120
Db 61 TTAATGTCCTGCTGCTTTTGTATAACGATAGGCAATGCTGTGGTCAATTTTAGCCCTTT 120

QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTAATTTTCTTAATTTGGCTATTCT 180
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTAATTTTCTTAATTTGGCTATTCT 180

QY 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG 240

QY 241 AATTTTGGAGTGGAAATCTGCAATGTTTTGGCTCAATTAAGTCAATCTTTTGTGCACAGCA 300
Db 241 AATTTTGGAGTGGAAATCTGCAATGTTTTGGCTCAATTAAGTCAATCTTTTGTGCACAGCA 300

QY 301 TCCGCTCTACAGTATTGTCCTCATTTAGCTAGCATCGATACGATCAGTTCAGTTCCTGCTGTG 360
Db 301 TCCGCTCTACAGTATTGTCCTCATTTAGCTAGCATCGATACGATCAGTTCAGTTCCTGCTGTG 360

QY 361 CGTTATAGACACAGACACTGGCATCTGGAATTTGCTCAAAATGTTGCTCAAAATGTTGTTGG 420
Db 361 CGTTATAGACACAGACACTGGCATCTGGAATTTGCTCAAAATGTTGCTCAAAATGTTGTTGG 420

QY 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480
Db 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGAGAACAGC 480

QY 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTACA 540
Db 481 ACCAAACACAGAGGAGTCGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTACA 540

QY 541 GCATTTCTGGAAATTCCTGCTCCCTGTCTCTGGTGGTCTATTTTCAAGTACAGATTAC 600
Db 541 GCATTTCTGGAAATTCCTGCTCCCTGTCTCTGGTGGTCTATTTTCAAGTACAGATTAC 600

QY 601 TGGAGCTGTGGAGCGTGGAGTCTCAGTAGGTGGCTAGCCCTAGCCAGCTGGATTCATCGCT 660
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Db 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCCAGCCAGCTGGGATTCATCGCT 660  
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Db 661 ACCTCTTCCAGGGCACTGGACACTCAGCAGAACTGGTGGCTTGTAGGACAAAGTCTT 720  
Qy 721 CCTGGATTAAGGAACACAGCCGCAATCCCTTCAATCAGAAATCCACGAGGAAAGAGCAGT 780  
Db 721 CCTGGATTAAGGAACACAGCCGCAATCCCTTCAATCAGAAATCCACGAGGAAAGAGCAGT 780  
Qy 781 CTCCTGGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840  
Db 781 CTCCTGGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840  
Qy 841 TTCTGCCGATCAGAAAGCCCAAGTCTTCCAGAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
Db 841 TTCTGCCGATCAGAAAGCCCAAGTCTTCCAGAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
Qy- 901 AGGAAGCTAGCAGGTCGCTAGCTGTCTCTCAGTGTCTTGGCAATTTGCTGGGCTCCG 960  
Db 901 AGGAAGCTAGCAGGTCGCTAGCTGTCTCTCAGTGTCTTGGCAATTTGCTGGGCTCCG 960  
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Db 1081 CCTTTGTGCCACAGAGCTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
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Db 1141 CCAGACCTTCACAGACCCAGTCAGTATCTTCTTGA 1176

RESULT 3  
US-10-626-398-6  
; Sequence 6, Application US/10626398  
; Publication No. US20050074841A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0034  
; CURRENT APPLICATION NUMBER: US/10/626,398  
; CURRENT FILING DATE: 2003-07-23  
; PRIOR FILING DATE: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: Patent in version 3.2  
; SEQ ID NO 6  
; LENGTH: 1176  
; TYPE: DNA  
; ORGANISM: Rattus rattus  
US-10-626-398-6

Query Match 100.0%; Score 1176; DB 21; Length 1176;  
Best Local Similarity 100.0%; Pred. No. 0;  
Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

Qy 1 ATGTCGGAGTCTAAGCGCACTGACGTCTTGCACTGCTGCTCAAGTCCCTTGGCAATT 60  
Db 1 ATGTCGGAGTCTAAGCGCACTGACGTCTTGCACTGCTGCTCAAGTCCCTTGGCAATT 60  
Qy 61 TTAATGTCCTGCTGCTTTGCTATACGATAGGCAATGCTGTGCTCATTTTACGCTTT 120

Db 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGCTCATTTTACGCTTT 120  
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180  
Qy 181 GACTTCTTGTGGGTGTCACTTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACGTG 240  
Db 181 GACTTCTTGTGGGTGTCACTTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACGTG 240  
Qy 241 AATTTTGGAAAGTGAATCTGTCATGTTTGGCTCAATTAAGTACTGACTATCTTTTGTGACAGCA 300  
Db 241 AATTTTGGAAAGTGAATCTGTCATGTTTGGCTCAATTAAGTACTGACTATCTTTTGTGACAGCA 300  
Qy 301 TCCGCTACAGTATTTGCTCTCATTTAGCTACGATCCGATACCCAGTCAAGTTCCTTCAAAAGCTGTG 360  
Db 301 TCCGCTACAGTATTTGCTCTCATTTAGCTACGATCCGATACCCAGTCAAGTTCCTTCAAAAGCTGTG 360  
Qy 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGCTCAANTGGTGGCTGTTTGG 420  
Db 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGCTCAANTGGTGGCTGTTTGG 420  
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Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAAAGC 480  
Qy 481 ACCAACAACAGAGGAGTGGCTTTGTTTACTGAGTGGTATCATCTCGCCATTAACA 540  
Db 481 ACCAACAACAGAGGAGTGGCTTTGTTTACTGAGTGGTATCATCTCGCCATTAACA 540  
Qy 541 GCATTTCTTGGAAATTTCTGCTCCCTGCTCTCTGCTGCTTGTGCTGTTTGTGCTGTTTGTAC 600  
Db 541 GCATTTCTTGGAAATTTCTGCTCCCTGCTCTCTGCTGCTTGTGCTGTTTGTGCTGTTTGTAC 600  
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Db 601 TGGAGCTGTGGAAAGCTGGAGTCTCAGTAGTGGCTCCTAGCCAGCTGGATTCATTCCT 660  
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Db 721 CCTGGATTAAGGAACACAGCCGCAATCCCTTCAATCAGAAATCCACGAGGAAAGAGCAGT 780  
Qy 781 CTCCTGGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840  
Db 781 CTCCTGGTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840  
Qy 841 TTCTGCCGATCAGAAAGCCCAAGTCTTCCAGAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
Db 841 TTCTGCCGATCAGAAAGCCCAAGTCTTCCAGAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
Qy 901 AGGAAGCTAGCAGGTCGCTAGCTGTCTCTCAGTGTCTTGGCAATTTGCTGGGCTCCG 960  
Db 901 AGGAAGCTAGCAGGTCGCTAGCTGTCTCTCAGTGTCTTGGCAATTTGCTGGGCTCCG 960  
Qy 961 TATTGCTGTTCACAAATTTCTTCAACTTATCGCAGAGGAGCGCCCCCAATCGAAT 1020  
Db 961 TATTGCTGTTCACAAATTTCTTCAACTTATCGCAGAGGAGCGCCCCCAATCGAAT 1020  
Qy 1021 TGGTACAGCAGTCTTGGCTACAGTGGTTCACATTCACATTAATCCCTTCTATAC 1080  
Db 1021 TGGTACAGCAGTCTTGGCTACAGTGGTTCACATTCACATTAATCCCTTCTATAC 1080  
Qy 1081 CCTTTGTGCCACAGAGCTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
Db 1081 CCTTTGTGCCACAGAGCTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
Qy 1141 CCAGACCTTCACAGACCCAGTCAGTATCTTCTTGA 1176  
Db 1141 CCAGACCTTCACAGACCCAGTCAGTATCTTCTTGA 1176

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RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Query Match      81.5%; Score 958.4; DB 20; Length 1176;
Best Local Similarity 88.4%; Pred. No. 5e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy      1  ATGTCGGAGTCTAACGGCACTGAGCGTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db      1  ATGTCGGAGTCTAACAGTACTGGCATCTTGGCCACCAGTCTCTCAGGTCCCTTGGCAATTT 60

Qy      61  TTAATGTCCTTGGTCTTGGTCTTAAACGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
Db      61  TTAATGTCCTTGGTCTTGGTCTTAAATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120

Qy      121  GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
Db      121  GTGTGGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180

Qy      181  GACTTCTTCGTGGGTGTCTCATTCCTCTGTACATCCCTCAGACGCTGTTTAACTGG 240
Db      181  GACTTCTTCGTGGGTGTGATTTCCATTCCTCTGTACATCCCTCAGAGTGTGTTAACTGG 240

Qy      241  AATTTTGAAGTGGAACTGCAATGTTTGGCTCATTAAGTCAATCTTTTGTGACAGCA 300
Db      241  AATTTTGAAGTGGAACTGCAATGTTTGGCTCATTAAGTCAATCTTTTGTGACAGCA 300

Qy      301  TCGTCTACAGATATTGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAAAGCTGTG 360
Db      301  TCGTCTACAAATATTGTCCTCATTTAGCTACGATCGATACCACTCAGTTTCAAAAGCTGTG 360

Qy      361  CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTGG 420
Db      361  TCTTATAGGCTCAACACACTGGCATCTGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420

Qy      421  ATACTGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAACAGC 480
Db      421  ATACTGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAACAGC 480

Qy      481  ACCAACACAGAGGAGTCGGAGCCTGGCTTTGTTACTGAGTGGTACATCCTCGCCATTACA 540
Db      481  ACGAACACAAAGGACTGTGAGCCTGGCTTTGTTACAGAGTGGTACATCCTCACCAATTACA 540

Qy      541  GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCCCTGGTGTCTAATTTCAAGTGTACAGATTAC 600
Db      541  ATGCTCTTGGAAATTCCTGCTCCCTGCTCATCTCTGTGGCTTATTTCAATGTACAGATTAC 600

Qy      601  TGGAGCCTGTGGAGCCTGGAGTCTCAGTAGGTGCTTACAGTGGTACCGCTGAGTTTCATCGCT 660
Db      601  TGGAGCCTGTGGAGCCTGAGGCTCTCAGTAGGTGCTTACAGTGGTACCGCTGAGTTTCATCGCT 660
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Db      661  ACCTCTTTCAGTCTCTTACAGGACACTTACACAGAGCTGGGGTGGCTTGCAGGACAAAGTAAT 720

Qy      721  CTTGGATTAAGGAACACAGCCGCATCCCTTTCATTTCAGAAAGTCCACGAGGAAAGAGCAGT 780
Db      721  CTTGGATTTGAAGGAATCAGCTGCATCTCTGTCACCTCAGAAAGTCTCTCGAAGAAAGAGCAGC 780

Qy      781  CTCTCGTGTCTTAAGGACTCAGATGAGCGGTAGTATCATCCCTTCAAAAGTGGGTTC 840
Db      781  ATCTCGTGTCTTAAAGGACTCAGATGAGCAGCAGTATCATCTGCTTCAAAAGTGGGTTC 840

Qy      841  TTCTGCGGATCAGAAAGCCAGTGTCTTACCACAGAGAGCACGCTGGAGCTTCTCAGAGGC 900
Db      841  TTCTGGGATCGAAAGTGTGAGCGCTTTCGCAAAAGGAGTACGAGAGCTTCTCAGAGGC 900

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Db      901  AGGAAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGGCCATTTTCTGGGTCCA 960

Qy      961  TATTGCTGTTCACAAATTTGTTCTTTCAACTTATCGAGAGGAGCGCCCCAAATCGATT 1020
Db      961  TACTGTCTGTTCACAAATTTGTTCTTTCAACTTATCGAGAGGAGCGCCCCAAATCGGTG 1020

Qy      1021  TGGTACAGCATAGCCTTTTGGCTACAGTGTTCAAATTTCACTTATTAATCCCTTCTATAC 1080
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Qy      1081  CCTTTGTGCCACAGACGTTTCCAGAAAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db      1081  CCTTTGTGTACAGGCGTTTCCAGAAAGGCTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140

Qy      1141  CGAGCACTTTCACAGACCCAGTCAGTATCTTCTTTGA 1176
Db      1141  CGAGCGCTGTACAGAACCCAGTCAGTATCTTCTTTGA 1176

RESULT 5
US-10-626-126-5
; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Query Match      81.5%; Score 958.4; DB 21; Length 1176;
Best Local Similarity 88.4%; Pred. No. 5e-295;
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

Qy      1  ATGTCGGAGTCTAACGGCACTGAGCGTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db      1  ATGTCGGAGTCTAACAGTACTGGCATCTTGGCCACCAGTCTCTCAGGTCCCTTGGCAATTT 60

Qy      61  TTAATGTCCTTGGTCTTGGTCTTAAACGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
Db      61  TTAATGTCCTTGGCTTGGCTTAAATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120

Qy      121  GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
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Db 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180
Qy 181 GACTTCTTCGTGGGTGTCTATCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTAACTGG 240
Qy 241 AATTTGGAGTGAATCTGATGTTTGGCTCAATTAAGTATCTGATCTATCTTTTGTGACAGCA 300
Db 241 AATTTGGAGTGAATCTGATGTTTGGCTCAATTAAGTATCTGATCTATCTTTTGTGACAGCA 300
Qy 301 TCCGTCTACAGTATGCTCTATAGCTACCATCGATACAGTACAGTTCGATTCGATTCGCTG 360
Db 301 TCTGTCTACAATATGCTCTATAGCTACCATCGATACAGTACAGTTCGATTCGATTCGCTG 360
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Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGGATTCATCGCT 660
Db 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGGATTCATCGCT 660
Qy 661 ACCTCTCCAGGGGCACTGGACACTCAGCAGAACTGGTGGCTTGTAGGACAGTCTT 720
Db 661 ACCTCTCCAGGGGCACTGGACACTCAGCAGAACTGGTGGCTTGTAGGACAGTCTT 720
Qy 721 CCTGGATTAAGGAACACAGCCGCTCTCTCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 721 CCTGGATTAAGGAATCAGCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 780
Qy 781 CTCTGTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCTTCAAAAGTGGTTCC 840
Db 781 ATCTGTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCTTCAAAAGTGGTTCC 840
Qy 841 TTCTGCCGATCAGAAAGCCGAGTCTTCCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
Db 841 TTCTGCCGATCAGAAAGCCGAGTCTTCCAGAGAGAGCAGTGGAGCTTCTCAGAGGC 900
Qy 901 AGGAAGCTTAGCAGTCTGCTAGTCTCTCTCTGAGTGTCTTGTGCAATTTGCTGGCTCCG 960
Db 901 AGGAAGCTTAGCAGTCTGCTAGTCTCTCTCTGAGTGTCTTGTGCAATTTGCTGGCTCCA 960
Qy 961 TATTGCTGTTCACAAATGTTCTTTTCAACTTATCCAGAGGGGAGCGCCCAAAATCGATT 1020
Db 961 TACTGTCTGTTCACAAATGTTCTTTTCAACTTATCCAGAGAGCGCCCAAAATCGGTG 1020
Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCATCTATTAATCCCTTCTATAC 1080
Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCATCTATTAATCCCTTCTCTGAC 1080
Qy 1081 CCTTTGTGCCACAGAGCTTTCCAGAAAGCTTTCTTGGAAAGATACTCTGTGTGACAAAGCAA 1140
Db 1081 CCTTTGTGTACAGGGCTTTCCAGAAAGCTTTCTTGGAAAGATACTTTTGTGTGACAAAGCAA 1140
Qy 1141 CCAGACCTTCCAGAGCCAGTCAAGTATCTTCTTGA 1176
Db 1141 CCAGCGCTGTCCAGAACCAAGTCAAGTATCTTCTTGA 1176
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US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5
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Query Match 81.5%; Score 958.4; DB 21; Length 1176;

Best Local Similarity 88.4%; Pred. No. Se-295;

Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

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Qy 1 ATGTCGGAGTCTAACGGCACTGACGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
Db 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCTTGGCATTT 60
Qy 61 TTAATGTCCTGCTTGGCTTGTCTTAAAGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
Db 61 TTAATGTCCTGCTTGGCTTGTCTTAAAGATAGGCAATGCTGTGGTCAATTTAGCCCTTT 120
Qy 121 GTACACAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGCTATTTCT 180
Db 121 GTGTGGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGCTATTTCT 180
Qy 181 GACTTCTTCGTGGGTGTCTATCCATTCCTCTGTACATCCCTCACACGCTGTTAACTGG 240
Db 181 GACTTCTTCGTGGGTGTGATTTCCATTCCTCTGTACATCCCTCACGTTGTTAACTGG 240
Qy 241 AATTTGGAGTGAATCTGCAATGTTTGGCTCAATTAAGTATCTGATCTATCTTTTGTGACAGCA 300
Db 241 AATTTGGAGTGAATCTGCAATGTTTGGCTCAATTAAGTATCTGATCTATCTTTTGTGACAGCA 300
Qy 301 TCCGCTCTACAGTATGCTCTATAGTACGATCGATACAGTACAGTTCGATTCGATTCGCTG 360
Db 301 TCTGTCTACAATATGCTCTATAGTACGATCGATACAGTACAGTTCGATTCGATTCGCTG 360
Qy 361 CGTTATAGACACAGCACACTGGCATCTGAAATATGTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATGTTGCTCAAAATGGTGGCTGTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGATTCGATTCGATTCGCTG 480
Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGATTCGATTCGATTCGCTG 480
Qy 481 ACCAACACAGAGGAGTGGAGCTGGCTTCTTACTAGTGGTACATCTCGCCATTACA 540
Db 481 ACGAACACAAAGGACTGTGAGCTGGCTTCTTACTAGTGGTACATCTCGCCATTACA 540
Qy 541 GCATTTCTTGGAAATTCCTGCTCCCTCTCTCTCTGTTGGTGTCTATTTCAAGTACAGATTTAC 600
Db 541 ATGCTCTTGGAAATTCCTGCTCCCTCTCTCTCTGTTGGTGTCTATTTCAAGTACAGATTTAC 600
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGGATTCATCGCT 660
Db 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTACGACGCTGGATTTCTCCACT 660
Qy 661 ACCTCTCCAGGGGCACTGGACACTCAGCAGAACTGGTGGCTTGTAGGACAGTCTT 720
Db 661 ACCTCTCCAGGGGCACTGGACACTCAGCAGAACTGGTGGCTTGTAGGACAGTCTT 720
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721	Qy	CTTGGATTAAAGAAACAGCGCGATCCCTTCAATTCAGAAAAGTCCAAGAGAAAGACGAGT	780
721	Db	CTTGGATTGAAGGAAATCAGCTGCATCTCGTCACTCAGAAAAGTCTCGAAGAAAGACGAGC	780
781	Qy	CTCCTGGTGCTTAAAGACTCACATGAGCGGTAGTATCATCGCCTTCAAGTGGGTTC	840
781	Db	ATCCTGGTGCTTAAAGACTCACATGAACAGCAGTATCATCGCCTTCAAGTGGGTTC	840
841	Qy	TTCTGCGGATCAGAAAAGCCAGTGCCTTCCACAGAGAGACGCTGGAGCTTCTCAGAGGC	900
841	Db	TTCTGCGATCGGAAAGTGACGCGTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC	900
901	Qy	AGGAAGCTAGCAGGTCCGTAGCTGTCTCTCAGATGCTTTTGGCATTTGCTGGGCTCCG	960
901	Db	AGGAAGCTAGCCAGGTCACCTGGCCATCCCTTCTGAGGCTTTTGCCATTTGCTGGGCTCCA	960
961	Qy	TATTTGCTGTTCACAATTGTCTTTTCAACTTATTCGACAGGGAGCGCCCAAAATCGATT	1020
961	Db	TACTGTCTGTTCACAATTGTCCCTTCAACTTACCCAGAACGGNACGCCCCAAATCGGTG	1020
1021	Qy	TGTTACAGCATAGCCTTTTGGCTTACAGTGGTCAAATTCATTAATATCCCTTCTATAC	1080
1021	Db	TGTTACAGCATTGCCTTCTGGCTGCAATGGTTCAAATTCGTTTGTTAATCCCTTCTGTAC	1080
1081	Qy	CCTTTGTGCCACAGACGTTTCCAGAGGCTTTCTGGAAGATACTCTCTGTGTGACAAAGCAA	1140
1081	Db	CCTTTGTGTACAGGCGTTTCCAGAGGCTTTCTGGAAGATACTCTTGTGTGACAAAGCAA	1140
1141	Qy	CCAGCACCTTTCACAGACCCAGTCAGTATCTCTTGA	1176
1141	Db	CCAGCGCTGTACAGAACCAAGTCAGTATCTCTTGA	1176

## RESULT 7

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US-09-812-216-1
; Sequence 1, Application US/09812216
; Patent No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-812-216-1

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Db	121	GTGGTGACAAAAACCTTAGACATCGAAGTAGTATATTTTTTCTTAACCTGGGCATCTCT	180
Qy	181	GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACATGG	240
Db	181	GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTCGAATGG	240
Qy	241	AATTTTGGAAAGTGGAAATCTGCATCTGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA	300
Db	241	GAITTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATATGTACAGCA	300
Qy	301	TCCGTCTACAGTATTTGTCCTCATTTAGTAGCATCGATCGATACCAAGTCAGTTTCAAAACGCTGTG	360
Db	301	TCTGTATATAACATTTGTCCTCATTCAGCTATGATCGATACCTGTCAAGTCTCAAAATGCTGTG	360
Qy	361	CGTTATAGACACAGACACACTGGCATCTCGAAAAATTTGTTGCTCAAAATGGTGGCTGTTTGG	420
Db	361	TCITTATAGAACTCAACATCTGGGCTCTGAAAGTTGTTACTCTGTATGGTGGCGGTTTGG	420
Qy	421	ATACTGGCTTCTTTGGTCAATGGCCCCAATGAATCTGGCTTCGGATTTCTTGGAAAGAACAGC	480
Db	421	GTGCTGGCTTCTTAGTGAATGGGCCAAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA	476
Qy	481	ACCAACACAGAGGAGTGGAGCTGGCTTGTGTACTCTGAGTGGTACATCTCTCGGCATTTACA	540
Db	477	- - TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTTGGCATCACA	534
Qy	541	GCATTTCTTGGAAATTCCTGCTCCCTGTCTCTGGTGGTCTATTTTCAGTGTACAGATTTAC	600
Db	535	TCATTTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGTTATTTTCAACATGAATATTTAT	594
Qy	601	TGGAGCTGTGGAAAGCGTGGGAGTCTCAGTAGGTGGCTTAGCCACGCTGGAATTCATCGCT	660
Db	595	TGGAGCTGTGGAAAGCGTGTATCATCTCAGTAGGTGGCCAAAGCCATCTCGACTGACTGCT	654
Qy	661	ACTCTTCCAGGGGCACTGGACACTCACGACAACTGGGTGGCTTGTAGGACAAAGTCCT	720
Db	655	GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT	714
Qy	721	CCTGGATTAAAGAAACGAGCGCATCCCTTCATTACAGAAAGTCCACGAGAAAGAGACGT	780
Db	715	TCTGCATCGACAGAGTTCTCTGCATCTTTTCAATTCAGAGAGACAGAGGAAAGAGTAGT	774
Qy	781	CTCTCTGTGTCTTTAAGGACTCATCATGAGCGGTAGTATCATTCGCTTTCAAAGTGGGTTC	840
Db	775	CTCATGTTTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC	834
Qy	841	TTCTGCCGATCAGAAAGCCAGTCTTCCACAGAGAGACAGCTGGAGCTTCTCAGAGGC	900
Db	835	TTCTCCCAATCAGATTCGTAGTCTTTCACCAAGGGGAACATGTTGAACCTGCTTAGAGCC	894
Qy	901	AGGAAGCTAGCCAGTCTGCTGCTCTCTGAGTGTCTTTTGGCAATTTGCTGGGCTCCG	960
Db	895	AGGAGATTAGCCAAAGTCACTGGCCATTTCTTAGGGGTTTTTGTCTTTGCTGGGCTCCA	954
Qy	961	TATTGCTGTTCACAAATGTTCTTTCAAATTATCGCAGAGGGAGCGCCCAAAATCGATT	1020
Db	955	TATTCTCTGTTCAAATTTGCTTTCATTTTATTTCTCAGCAACAGGCTCTTAAATCAGTT	1014
Qy	1021	TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAAATTCATTTAATCCCTTCTATAC	1080
Db	1015	TGGTATAGAAATGGATTTTGGCTTTCAGTGGTTCAAATTCCTTTGTCAATCCCTTTTGTAT	1074
Qy	1081	CTTTGTGCCACAGACGTTTTCCAGAAAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA	1140
Db	1075	CCATTGTGTACAAAGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATAAAAAAGCAA	1134
Qy	1141	CCAGCACTTC- - -ACAGACCCAGTCAGTATCTTCTTGA	1176
Db	1135	CCTCTACCATCACAAACACAGTCGGTCTAGTATCTTCTTAA	1173

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US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derk
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiatong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: FastSeq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapien
US-09-910-411-1

Query Match          56.9%; Score 669; DB 9; Length 1173;
Best Local Similarity 74.2%; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGCGGAGTCTAACGGCACTGACGCTGTGCGCACTGACTGCTCAAGTCCCTTGCGCAATT 60
Db 1 ATGCGAGATATAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATT 60
Qy 61 TTAATGCTCCCTGCTTGTCTTTGCTTATACGATAGGCAATGCTGTGCTTATAGCCTTT 120
Db 61 TTTATGCTCTTAGTGTCTTTGCTTATATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCT 180
Qy 181 GACTTCTTGTGGGTGTCATCCATTCCTCTGTACATCCCTCAAGCTGTTTAACTGG 240
Db 181 GACTTCTTGTGGGTGTCATCCATTCCTTGTACATCCCTCAAGCTGTTTAACTGG 240
Qy 241 AATTTTGGAGTGAATGCTGATCTTTTGGCTCACTACTGACTATCTTTTGTGCACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
Qy 301 TCCGCTCTACAGTATTGCTCTCATTTAGCTTACGATCGATACCACTCAGTTTCAAACGCTGTG 360
Db 301 TCTGTATATAACATTGCTCTCATCGATGATGATCGATACCTGTGACTCTCAATGCTGTG 360
Qy 361 CGTTATAGACACAGCACTGGCATCCTGAAATTTGTGCTCAAATTTGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
Qy 421 ATACTGCTTTCTTGGTCAATGGGCCCAATGATTCTGGCTCGGATTTCTTGAAGAACAGC 480
Db 421 GTGCTGGCTCTTCTTAGTGAATGGGCCAATGATTCTTAGTTTCAGAGTCTTGAAGAA 476
Qy 481 ACCAACACAGAGGAGTGGAGCCTGGCTTCTTACTGAGTGGTATCTCTCGCCATTACA 540
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGNAUGGTATACCTTGGCCATACA 534
Qy 541 GCATTCTTGGAAATCTCTGCTCCCTGCTCTTGTGGTGTCTATTTTCAAGTGTACAGATTAC 600
Db 535 TCATTCTTGGAAATCTGTGATCCAGTCACTTTAGTGGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCCCTAGCCAGGCTGGATTCTATCGCT 660
Db 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTCCCTAGCCAGGCTGGATTCTATCGCT 660

US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131

RESULT 9
US-09-875-076-13
; Sequence 13, Application US/09875076
; Publication No. US20030017528A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/09/875,076
; CURRENT FILING DATE: 2001-06-06
; PRIOR APPLICATION NUMBER: 09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
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/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/141,448
/ PRIOR FILING DATE: 1999-06-29
/ PRIOR APPLICATION NUMBER: 60/156,653
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,633
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,555
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/156,634
/ PRIOR FILING DATE: 1999-09-29
/ PRIOR APPLICATION NUMBER: 60/157,280
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,294
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,281
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,293
/ PRIOR FILING DATE: 1999-10-01
/ PRIOR APPLICATION NUMBER: 60/157,282
/ PRIOR FILING DATE: 1999-10-01
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: Patent In Ver. 2.1
/ SEQ ID NO 13
/ LENGTH: 1173
/ TYPE: DNA
/ ORGANISM: Homo sapiens
US-09-875-076-13

Query Match      56.9%; Score 669; DB 10; Length 1173;
Best Local Similarity 74.2; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy      1  ATGTCGGAGCTTAAGGCACTGAGCTCTGGCACTGACTGCTCAAGTCCCTTGGCAATTT 60
Db      1  ATGCCAGATATAATGACCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60

Qy      61  TTAATGTCCTGCTGCTGCTTTGCTATACGATAGCAATGCTGTGGTCAATTTTAGCCCTTT 120
Db      61  TTTATGTCCTTAGTAGCTTTGCTATATAGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120

Qy      121  GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db      121  GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTTAACTTGGCCATCTCT 180

Qy      181  GACTTCTCTGGGTGTCATCTCAATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
Db      181  GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 240

Qy      241  AATTTTGGAAAGTGAATCTGCATGTTTTGGTCTATTACTGACTATCTTTTGTGCACAGCA 300
Db      241  GAATTTGGAAAGGAATCTGTGATTTTGGTCTACTACTGACTATCTTTTGTACAGCA 300

Qy      301  TCCGTCTACAGTATTGTCCTCATTAGCTAGCATGATACGATCAGTCAAGTCAAGTCTG 360
Db      301  TCTGTATATAACATTGTCCTCATCAGCTATGATCATACCTGTGAGTCAAAATGCTGTG 360

Qy      361  CGTTATAGACACAGCACATCGGCATCTGGAATTTGTTGCTCAAAATGGTGGCTGTTGG 420
Db      361  TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTTACTCTGTATGGTGGCGTGG 420

Qy      421  ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTGGGATTTCTTGAAGAACAGC 480
Db      421  GTGCTGGCTTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCTAGAGTCTTGAAGAA---- 476

Qy      481  ACCAACACAGAGGAGTGGAGCCCTGGCTTTGTTTACTGAGTGGTACATCCTCGCCATTACA 540
Db      477  --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTTCGGAAATGATACATCTTGGCCATACA 534

Qy      541  GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTTCAAGTGTACAGATTAC 600
Db      535  TCATTTCTTGGAAATTCGTGATCCCAAGTCATCTTAGTCGCTTATTTTCAACATGAATATTAT 594
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Qy      601  TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGCCCTAGCCACGCTGGATTCATCGCT 660
Db      595  TGGAGCTGTGGAAGCGTGTATCATCTCAGTAGTGCCTCAAGCCATCTCTGAGTACTGCT 654

Qy      661  ACCTTTCCAGGGGCACTGGACACTCACGACAACTGGGTGGCTTTGTAGGACAAGTCTTT 720
Db      655  GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTTCAAGGAGATCTCTT 714

Qy      721  CTTGGATTAAGGAAACAGCCGCATCCCTTCATTTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db      715  TCTGCATCGACAGAAGTTCTCTGCATCTCTTTCATTTCAGAGAGACAGAGGAGAAAGTAGT 774

Qy      781  CTCTGCTGTCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840
Db      775  CTCAATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834

Qy      841  TTCTGCCGATCAGAAAGCCAGTGTTCACAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Db      835  TTCTCCAAATCAGATTTCTGTAGCTTTCACAAAGGGAACATGTTGAACTGCTTTAGAGCC 894

Qy      901  AGGAAGTAGCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 960
Db      895  AGGAGATTAGCCAAAGTCACTGGCCATTTCTTTAGGGGTTTTTCTGTTGCTGGGCTCCA 954

Qy      961  TATTGCTGTTCACAAATTTGTTCTTTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db      955  TATTCTCTGTTTCAAAATTTGCTTTTCAATTTTATTTCTCAGCAACAGGTCTCTAATCAGTT 1014

Qy      1021  TGGTACAGCATAGCCTTTTGGCTTACAGTGGTTCAAATTCATTTCACTTATTAATCCCTTTTATATC 1080
Db      1015  TGGTATAGAATTTGCAATTTTGGCTTCAAGTGGTTCAAATTCCTTTCTCAATCCCTTTTGTAT 1074

Qy      1081  CTTTGTGTCACAGAGTTCACAGAAAGGCTTTCTGGAAGGCTTTCTGGAAGTACTCTGTGTGACAAAGCAA 1140
Db      1075  CCATTGTGTCACAGGCTTTCAAAAGGCTTTCTTGAATAATATTTTGTATATAAAAGCAA 1134

Qy      1141  CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176
Db      1135  CCTCTACCATCACAAACAGTCGGTCAGTATCTTCTTAA 1173
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## RESULT 10

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US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
```





; CURRENT APPLICATION NUMBER: US/10/052.193  
; CURRENT FILING DATE: 2002-01-17  
; PRIOR APPLICATION NUMBER: 0101223.6  
; PRIOR FILING DATE: 2001-01-17  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-052-193-1

Query Match 56.9%; Score 669; DB 13; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 1.7e-202;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
  
QY 1 ATGTCGAGCTTAACCGGCACTGAGCTCTTCCCACTGCTCAAGTCCCTTTGGCAATTT 60  
DB 1 ATGCCAGATACTAATAGCACAATCAATTTATCTAAGCACTCGTGTACTTTAGCAATTT 60  
  
QY 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 61 TTTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
  
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180  
DB 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCTATTCT 180  
  
QY 181 GACTTCTTCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GACTTCTTCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
  
QY 241 AATTTTGAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 241 AATTTTGAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
  
QY 241 GATTTTGAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
DB 241 GATTTTGAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
  
QY 301 TCCGCTCAGAGTATGTCCTCATTAGCTAGCATCGATCGATCGATCGATCGATCGATCGAT 360  
DB 301 TCCGCTCAGAGTATGTCCTCATTAGCTAGCATCGATCGATCGATCGATCGATCGATCGAT 360  
  
QY 361 CGTTATAGACACAGCAGCAGCTGCGATCCTGAAATTTGCTGCTGCTGCTGCTGCTGCTGCT 420  
DB 361 TCTTATAGAACTCAACATCTGCGGTCTTGAAGATTGTTACTCTGATGGTGGCGGTTTGG 420  
  
QY 421 ATACTGCTTCTTGTGCTCAATGGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 421 GTGCTGCTTCTTGTGCTCAATGGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
  
QY 481 ACCAACAACAGAGGAGTGGAGCCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTAC 540  
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCGCCATTAC 534  
  
QY 541 GCATTTCTGAAATTCCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 535 TCATTTCTGAAATTCCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 594  
  
QY 601 TGGAGCTGTGGAGCCTGGAGTCTCAGTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
DB 595 TGGAGCCTGTGGAGCCTGGATCTCATCTCAGTAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCT 654  
  
QY 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGAACTGGGTGGCTGTAGGACAACTCTT 720  
DB 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
  
QY 721 CTTGGATTAAGGAACAGCGGCAATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGGAGT 780  
DB 715 TCTGCATCGAAGAGTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 774  
  
QY 781 CTCTGCTGCTTAAAGGACTCAGATGCGGTAGTATCATCGCTTCAAGTGGGTTC 840  
DB 775 CTATGTTTTCTTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCAAAATGGGTTC 834  
  
QY 841 TTCTGCCGATCAGAAAGCCAGTCTCTTCAACAGAGAGCAGTGGAGCTTCTCAGAGGC 900

DB 835 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATCTTGAACCTGCTTAGAGCC 894  
QY 901 AGGAAGCTAGCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
DB 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTCTGTTGCTGGGTCCA 954  
QY 961 TATTGCTGTTCACAATTTGTTCTTTCAACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020  
DB 955 TATTGCTGTTCACAATTTGTTCTTTCAACTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014  
QY 1021 TCGTACAGCATAGCCTTTTGGCTACAGTGGTTCATTTCACTTATTAATCCCTTTCTATAC 1080  
DB 1015 TGGTATAGAAATTCATTTTGGCTTCAAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074  
QY 1081 CTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATATCTGCTGTCGACAAAGCAA 1140  
DB 1075 CCATTGTGTCAAGGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134  
QY 1141 CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTGA 1176  
DB 1135 CCTTACCATCAACACACAGTCGGTCAGTATCTTCTTAA 1173

## RESULT 12

US-10-290-078-26  
; Sequence 26, Application US/102900078  
; Publication No. US20030124596A1  
; GENERAL INFORMATION:  
; APPLICANT: Carroll, Joseph A.  
; TITLE OF INVENTION: Methods and Compositions for Treating  
; Hematological Disorders Using 232, 2059, 10630, 12848, 13875,  
; TITLE OF INVENTION: 14395, 14618, 17692 or 58874  
; FILE REFERENCES: MPI2001-288P1(M)  
; CURRENT APPLICATION NUMBER: US/10/290, 078  
; NUMBER OF SEQ ID NOS: 27  
; CURRENT FILING DATE: 2002-11-07  
; SOFTWARE: FastSeq for Windows Version 4.0  
; SEQ ID NO 26  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo Sapien  
; FEATURE:  
; NAME/KEY: CDS  
; LOCATION: (1)...(1173)  
US-10-290-078-26

Query Match 56.9%; Score 669; DB 15; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 1.7e-202;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
  
QY 1 ATGTCGAGCTTAACCGGCACTGAGCTCTTCCCACTGCTCAAGTCCCTTTGGCAATTT 60  
DB 1 ATGCCAGATACTAATAGCACAATCAATTTATCTAAGCACTCGTGTACTTTAGCAATTT 60  
  
QY 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 61 TTTATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
  
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180  
DB 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180  
  
QY 181 GACTTCTTCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
DB 181 GACTTCTTCTGGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 240  
  
QY 241 AATTTTGAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 241 AATTTTGAAGTGAATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
  
QY 301 TCCGCTCAGAGTATGTCCTCATTAGCTAGCATCGATCGATCGATCGATCGATCGATCGAT 360  
DB 301 TCCGCTCAGAGTATGTCCTCATTAGCTAGCATCGATCGATCGATCGATCGATCGATCGAT 360

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Db 301 TCTGTATATAACATTGTCCTCATCAGCTATGATCGATACCTGTCAAGTCTCAAAATGCTGTG 360
Qy 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTTGAAGATTGTTACTCTGATGGTGGTGGTGG 420
Qy 421 ATACTGCTTTCTTGGTCAATGGCCCAATGATTTGCTGGCTTGGATTTCTTGGAAAGACAGC 480
Db 421 GTGCTGGCTTCTTGTAGTGAATGGCCCAATGATTTCTAGTTTCTAGAGTCTTGGAAAGAA 476
Qy 481 ACCAAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCCGCTCCATACAA 540
Db 477 --TGAAGGTAGTGAATGTAACCTTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 541 GCATTTCTTGAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGAATTCGTTGATCCCAAGTCATCTTAGTGGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCTTAGCCAGCCAGCTGATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCTTAGCCAGCCATCTTGGACTGACTGCT 654
Qy 661 ACCTTTCCAGGGGCACTGGACACTCAGCAGACTCGGTTGGCTTGTAGACAAAGTCTT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTAAAGGAACAGCGGCATCTCCTTCATTCAGAAAGTCCACAGGAGAAAGAGAGT 780
Db 715 TCTGATCGACAGAAAGTCTCGATCTCTTCATTCAGAGAGCGGAGGAGAGAGTAGT 774
Qy 781 CTCTGTGTCTTAAAGACTCAGATGAGCGGTAGTATCATCGCTTCAAAGTGGGTTC 840
Db 775 CTATGTTTTCTCAAGAACCAAGATGAATAGCAATACAATTGCTTCCAAAATGGGTTC 834
Qy 841 TTCTCGGATCAGAAAGCCAGTCTTCCAGAGAGAGCAGCGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCGTAGCTCTTCCAAAGGAAACATGTTGAACCTCTTAGAGCC 894
Qy 901 AGAAGCTAGCCAGTCTGCTGCTGAGTCTCTTGGCCATTTGCTGGGCTCCG 960
Db 895 AGGAGATTAGCCAGTCTAGTCTCTTGGGCTCTTGGGCTCTTGGGCTCCCA 954
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTGTTCACAAATGTTCTTCACTTTTATTCCTCAGCAACAGGCTCTTAATCAGTT 1014
Qy 1021 TGGTACAGATAGCTTTTGGCTACAGTGGTCAATTCATTTAATCCCTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGGTCAATTTCTTGTCAATCTCTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGACGCTTTCCAGAGGCTTTCTGGAAGATACCTCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTACAGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATAAAGAAAGCAA 1134
Qy 1141 CCAGCACTTC---ACAGCCAGTCTAGTATCTTCTTGA 1176
Db 1135 CCTCTACCATCACAAACACAGTGGTCTAGTATCTTCTTAA 1173
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## RESULT 13

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US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; CURRENT FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
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; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13
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Query Match 56.9%; Score 669; DB 15; Length 1173;
Best Local Similarity 74.2%; Pred. No. 1.7e-202;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGCTGTGCCACTGCTCAAGTCCCTTGGCATTT 60
Db 1 ATGCCAGATACTAATACACAAATCAATTTATCACTAGCACTCGTGTACTTTAGCATTT 60
Qy 61 TTAATGTCCTGCTGCTTTTGTATTAACGATAGGCAATGCTGTGGTCATTTAGCCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATTAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db 121 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTTCTGGGTGTCTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
Db 181 GACTTCTTCTGGGTGTCTCATCTCCATTCCTTGTACATCCCTCACAGCTGTTTGAATGG 240
Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTGTGCTCATTAATGCTATCTTTTGTGACAGCA 300
Db 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 301 TCGTCTACAGTATTGTCCTCATTTAGCTACGATCGATACAGTTCAGTTTCAAAAGCTGTG 360
Db 301 TCTGTATATAACATGTCCTCATCAGCTATGATCGATACCTGTCAAGTCTCAATGCTGTG 360
Qy 361 CGTTATAGACACAGCACACTGGCATCTGGAATTTGTTACTGAGTGGTACATCTCGCCATACA 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTCTGAGATTGTTACTCTGATGGTGGCCGTTGG 420
Qy 421 ATACTGCTTTCTTGGTCAATGGCCCAATGATTTCTGCTGCTGGATTTCTTGGAAAGACAGC 480
Db 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCTAGAGTCTTGGAAAGAA 476
Qy 481 ACCAAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATACA 540
Db 477 --TGAAGGTAGTGAATGTAACCTTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 541 GCATTTCTTGAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGAATTCGATGATCCCAAGTCACTTAGTGGCTTATTTTCAACATGAATTTAT 594
Qy 601 TGGAGCTGTGGAAGCTGGAGTCTCAGTAGTGGCTTAGCCAGCCAGCTGATTCATCGCT 660
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595 TGGAGCTGTGGAAGCGTGATCATCTCAGTAGGTGCAAGCCATCTTGAGCTGACTGCT 654  
661 ACCTCTTCAGGGGCACTGAGCACTCAACGAGAACTGGGTGGCTGTGAGCAAGTCTTT 720  
655 GTCTCTTCCAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
721 CTTGGATTAAAGGAACACAGCGCATCCCTTCATTTCAGAAAGTCCACGAGGAAGAGCAGT 780  
715 TCTGCATCGACAGAGTCTCGCATCTCTTCATTTCAGAGAGACAGAGGAGAAAGAGTAGT 774  
781 CTCTCGGTGTCTTAAGGACTCACATGAGCGGTAGTATCATCGCTTTCAAAAGTGGGTTC 840  
775 CTCATGTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTTC 834  
841 TTCTGGGATCAGAAAGCCAGTGTTCACACAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
835 TTCTCCCAATCAGATTCTGTAGCTCTTCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
901 AGGAAGCTAGCCAGGTGCTAGTGTCTCTCAGTGTCTTTTGGCATTTTGGCTGGCTCCG 960  
895 AGAGATTAGCCAAAGTCACTGGGCATCTCTTAGGGGTTTTTGTGTTTGTCTGGGTCCA 954  
961 TATTGCTGTTCACAAATGTTTTCACAACTTATCGCAGAGGGGAGCGGCCCAAAATCGATT 1020  
955 TATTCTGTTCACAAATGTTTTCATTTTATTCCTCAGCAACAGGTCCCTAAATCAGTT 1014  
1021 TGTACAGCATAGCTTTTGGCTACAGTGTTCACATTCATTAATTCCTTATATTCCTTATAC 1080  
1015 TGGTATAGAAATTCGATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTGTAT 1074  
1081 CCTTTGGCCACAGAGCTTTCCAGAGGCTTCTGGAAGTATCTCTGTGTGACAAAGCAA 1140  
1075 CCATTGTGTCAAGGCGCTTTCAAAAGGCTTCTTGAAATATTTTGTATAAAAGGCAA 1134  
1141 CCAGCACCTTC---ACAGACCCAGTCAAGTATCTTCTTGA 1176  
1135 CCTTACCACACACACAGTCCGTGATCTTCTTAA 1173

## RESULT 14

US-10-354-769-1  
; Sequence 1, Application US/10354769  
; Publication No. US20030149242A1  
; GENERAL INFORMATION:  
; APPLICANT: Pfizer Inc.  
; APPLICANT: O'Reilly, Mark A.  
; APPLICANT: Peter, Beate  
; TITLE OF INVENTION: NOVEL POLYPEPTIDE  
; FILE REFERENCE: PC10373B  
; CURRENT APPLICATION NUMBER: US/10/354,769  
; CURRENT FILING DATE: 2003-01-30  
; PRIOR APPLICATION NUMBER: US 09/698,801  
; PRIOR FILING DATE: 2000-10-27  
; PRIOR APPLICATION NUMBER: US 60/211,243  
; PRIOR FILING DATE: 2000-06-14  
; PRIOR APPLICATION NUMBER: GB 9925641.4  
; PRIOR FILING DATE: 1999-10-29  
; PRIOR APPLICATION NUMBER: GB 0009973.9  
; PRIOR FILING DATE: 2000-04-20  
; NUMBER OF SEQ ID NOS: 10  
; SOFTWARE: PatentIn version 3.1  
; SEQ ID NO 1  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-354-769-1

Query Match 56.98; Score 669; DB 15; Length 1173;

Best Local Similarity 74.2; Pred. No. 1.7e-202;

Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

1 ATGTGGAGTCTAACGGCACTGACGTCTTGCCACTGCTCAAGTCCCGCTTGGCATTT 60

1 ATGCCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
61 TTAATGTCCTGCTGCTTTTGGCTATAAGATAGGCAATGCTGTGTGCTCAATTTAGCCTTT 120  
61 TTTATGCTCTAGTAGCTTTTGGCTATAAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120  
121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTGGCTATTCTTCT 180  
121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTCTTAATCTTGGCCATCTCT 180  
181 GACTTCTCTGGTGGTGTCTATCTCCATCTCTGTATACATCCCTCACACGCTGTTTAACTGG 240  
181 GACTTCTTGTGGTGTGTATCTCCATCTCTTGTATCATCCCTCACACGCTGTTTAACTGG 240  
241 AATTTTGGAAAGTGAATCTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGCAAGCA 300  
241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTTATGTACAGCA 300  
301 TCGTCTACAGTATTTGCTCTCATTTAGCTACGATCGATCCAGTCACTTCAAAAGCTGTG 360  
301 TCTGTATATAACATTTGCTCTCATCTCAGCTATGATCGATACCTGTCAGTCTCAAAAGCTGTG 360  
361 CGTTATAGAGCACAGCACACTTGGCATCTGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420  
361 TCTTATAGAACTCAACATCTGCGGTCTTGAAGATTTGTTACTCTGATGGTGGCCGTTGG 420  
421 ATACTGGCTTTCTTGTGTCAATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 480  
421 GTGCTGGCTTCTTGTGTGAATGGGCAATGATTTCTAGTTTTCAGAGTCTTTGGAAGGA--- 476  
481 ACCAACACAGAGAGGCGAGCGCTGCTGTTGTTACTGAGTGGTACATCTCCGCAATPACA 540  
477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 534  
541 GCATTTCTTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTCTATTTTCAAGTGTACAGATTAC 600  
535 TCATTTCTTGGAAATCTCTGATCCCGATCACTTAGTCTGCTTATTTCAACATGAATATTAT 594  
601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTAGCCAGTGTGATTCATCGCT 660  
595 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTAGCCAGTGTGATTCATCGCT 654  
661 ACCTCTTTCAGGGGCACTGAGCACTCAGCAGAACTGGGTGGCTTGTAGGACAAAGTCTT 720  
655 GTCTCTTCAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
721 CCTGGATTAAAGGAACACAGCGCATCCCTTCATTTCAGAAAGTCCACGAGGAAGAGCAGT 780  
715 TCTGCATCGACAGAGTCTCGCATCTCTTTCATTTCAGAGAGACAGAGGAGAAAGAGTAGT 774  
781 CTCTGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840  
775 CTCATGTTTTCTTCAAGAAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTTC 834  
841 TTCTGGGATCAGAAAGCCAGTGTTCACACAGAGAGACAGTGGAGCTTCTCAGAGGC 900  
835 TTCTCCCAATCAGATTCTGTAGCTCTTTCACCAAGGGAACATGTTGAACCTGTTAGAGCC 894  
901 AGGAAGCTAGCCAGGTGCTGCTGCTCTCTGAGTGTCTTTTGGCATTTTGGCTGGCTCCG 960  
895 AGGAGATTAGCCAAAGTCACTGGGCATCTCTTAGGGGTTTTTGTGTTTGTCTGGGTCCA 954  
961 TATTGCTGTTCACAAATGTTTTCATTCATTCAGCAGAGGGGAGCGGCCCAAAATCGATT 1020  
955 TATTCTGTTCACAAATGTTTTCATTTTATTCCTCAGCAACAGGTCCCTAAATCAGTT 1014  
1021 TGTACAGCATAGCTTTTGGCTACAGTGTTCACATTCATTAATTCCTTATATTCCTTATAC 1080  
1015 TGGTATAGAAATTCGATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTGTAT 1074  
1081 CCTTTGGCCACAGAGCTTTCCAGAGGCTTCTGGAAGTATCTCTGTGTGACAAAGCAA 1140

Db 1075 CCAATGCTCACAGCGCTTTCAAAAGCGTTCTTGAATAATATTTTGTATAAAAGCAA 1134  
Qy 1141 CCAGCACCTTC---ACAGACCAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1173

RESULT 15  
US-10-393-807-13  
; Sequence 13, Application US/10393807  
; Publication No. US20030175891A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/10/393,807  
; CURRENT FILING DATE: 2003-03-21  
; PRIOR APPLICATION NUMBER: US/09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/109,213  
; PRIOR FILING DATE: 1998-11-20  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,437  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,439  
; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/136,567  
; PRIOR FILING DATE: 1999-05-28  
; Remaining Prior Application data removed - See File Wrapper or PALM.  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
US-10-393-807-13

Query Match 56.9%; Score 669; DB 16; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 1.7e-202;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGACGCTCTTGGCACTGCTCAAGTCCCTTGGCAATT 60  
Db 1 ATGCCAGATATAATAGCACAACTAAATTTATCATCAAGCACTCGGTGTACTTTAGCAATT 60  
Qy 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGGCAATGCTGTGCTCAATTTTAGCCTTT 120  
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGCTCAATTTTAGCCTTT 120  
Qy 121 GTAGCAGACAGAAACCTTTAGACATCGAAGTAAATATTTTCTTAAATTTGGCTATTTCT 180  
Db 121 GTGGTGGACAAAACCTTTAGACATCGAAGTAAATATTTTCTTAACTTGGCCATCTCT 180  
Qy 181 GACTTCTTCGGGTGCTCATCTCCATCTCTGTACATCCCTCAACGCTGTTTAACTGG 240  
Db 181 GACTTCTTTGGGTGCTCATCTCCATCTCTTTGTACATCCCTCAACGCTGTTTGAATGG 240  
Qy 241 AATTGGAAGTGAATCTGCGATGTTTGGGCTCATTTAGTACTATCTTTTGTGACAGCA 300  
Db 241 GATTTTGGAAAGGAATCTGTGATTTGGGCTCACTACTGACTATCTGTATGTATACGA 300

Search completed: August 5, 2005, 15:08:29  
Job time : 781 secs

Qy 301 TCCGCTTACAGTATTTGCTCTCATTTAGCTACGATCGATACCACTAGTCTTCAAAACGCTGTG 360  
Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATGATACCTGTGCTCAGTCTCAATGCTGTG 360  
Qy 361 CGTTATAGACACAGCACACCTGCGCATCTGAAAATTTGTTGCTCAAAATGCTGCTGTTGG 420  
Db 361 TCTTATAGAACTCAACATACTGGGGCTTTGAAGATTTGTTACTCTGTGATGGTGGCCGTTGG 420  
Qy 421 ATACTGGCTTTCTTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTTGAAAGAACAGC 480  
Db 421 GTGCTGGCTTTCTTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTTGGAAGGA--- 476  
Qy 481 ACCAACACAGAGGAGTGGAGCCTGGCTTTGTTACTAGTGGTACATCTCGCCCATAC 540  
Db 477 --TGAAGGTAGTGAATGTGAACCTTGGATTTTTTTCGGAATGGTACATCTTTGCCATCACA 534  
Qy 541 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTTGGTGGTCTATTTTCAGTGTACAGATTTAC 600  
Db 535 TCATTTCTTGGAAATTCGTTGATCCAGTCTATCTTAGTCGCTTATTTCAACATGAATATTTAT 594  
Qy 601 TGGAGCCTGTGGAAAGCGTGGAGTCTCAGTAGGTGCTCCCTAGCCAGCTGGATTTCACTGCT 660  
Db 595 TGGAGCCTGTGGAAAGCGTGTATCTCAGTAGGTGCTCCAAAGCCATCTCTGGACTGACTGCT 654  
Qy 661 ACCTCTTCCAGGGGCACTGGACACCTACGAGAACTGGGTTGGCTTTAGGACAAAGTCTTT 720  
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTACAGAGGTAGACTATCTTTCAAGGAGATCTCTT 714  
Qy 721 CCTGGAATTAAGGAACAGCCGCTCTCTTCAATCAGAAAGTCCACAGGAGAAAGAGCAGT 780  
Db 715 TCTGCATCGACAGAAAGTTCTGTCATCTTTTCAATCAGAGACAGAGAGAAAGAGTAGT 774  
Qy 781 CTCCTGCTGTCTTTAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840  
Db 775 CTGATGTTTCTCAAGAACCAAGTGAATAGCAATACAAATGCTTCCAAATGGGTTC 834  
Qy 841 TTCTGCCGATCAGAAAGCCGCTGCTTCCAGAGAGAGACGCTGGAGCTTCTTCAGAGGC 900  
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
Qy 901 AGGAAGCTAGCCAGTCTGCTAGCTGCTCTGCTGAGTGTCTTTGCCATTTGCTGGGCTCG 960  
Db 895 AGGAGATTAGCCAAAGTCACTGGCAATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954  
Qy 961 TATTGCTGTTTCAAAATTTGTTCTTTCAACTTATCGCAGAGGGGAGCGCCCAAAATCGATT 1020  
Db 955 TATTCTGTTTCAAAATTTGTTCTTTTCAATTTATTTCTCAGCAACAGGTCCTTAAATCAGTT 1014  
Qy 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAGTCACTTATTAATCCCTTTCTATAC 1080  
Db 1015 TGGTATAGAAATGCAATTTTGGCTTTCAGTGGTTCAAATTCCTTTGTCAATCCTCTTTGTAT 1074  
Qy 1081 CCTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
Db 1075 CCATTTGTCTCAAGAGCTTTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAGCAA 1134  
Qy 1141 CCAGCACCTTC---ACAGACCAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCATCAACACAGTCGGTCAGTATCTTCTTAA 1173

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

Run on: August 5, 2005, 07:43:43 ; Search time 654 Seconds  
(without alignment)  
10644.672 Million cell updates/sec

Title: US-10-626-126-6

Perfect score: 1176

Sequence: 1 atgtcggagtctaaggcac.....cccagtcagtcattcttctga 1176

Scoring table: IDENTITY NUC

Gapop 10.0 , Gapext 1.0

Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : N Geneseq 16Dec04.\*

1: geneseqn1980s.\*

2: geneseqn1990s.\*

3: geneseqn2000s.\*

4: geneseqn2001as.\*

5: geneseqn2001bs.\*

6: geneseqn2002as.\*

7: geneseqn2002bs.\*

8: geneseqn2003as.\*

9: geneseqn2003bs.\*

10: geneseqn2003cs.\*

11: geneseqn2003ds.\*

12: geneseqn2004as.\*

13: geneseqn2004bs.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

# SUMMARIES

Result No.	Score	Query Match	Length	DB ID	Description
1	1176	100.0	1176	6	AAI70982 Rat hist
2	958.4	81.5	1176	6	AAI70981 Mouse his
3	958.4	81.5	1538	12	ADO30257 Mouse GPC
4	670.6	57.0	1173	6	AAI67750 Human his
5	669	56.9	1173	3	AAA46023 Human G p
6	669	56.9	1173	3	AAI67750 Human his
7	669	56.9	1173	3	AAI67750 Human his
8	669	56.9	1173	5	AAH24007 Human G p
9	669	56.9	1173	6	ABZ80663 Human his
10	669	56.9	1173	6	ABQ78739 Nucleotid
11	669	56.9	1173	6	AAI70980 Human his
12	669	56.9	1173	8	ACA93262 Human cDN
13	669	56.9	1173	10	ADG98759 Human orp
14	669	56.9	1173	10	ABSS7063 Human cDN
15	669	56.9	1173	11	ADJ26922 Human end
16	669	56.9	1173	12	ADG86374 Human end
17	669	56.9	1173	12	ADJ88375 Novel hum
18	669	56.9	1173	12	ADP20167 Human G p
19	669	56.9	1173	12	ADQ75073 Human cDN
20	669	56.9	1227	4	AAI66009 Human GPR

21	669	56.9	1265	6	AAS98078 Human DNA
22	669	56.9	1265	9	AAD55125 Human H4
23	669	56.9	1266	6	ABK12959 DNA seque
24	669	56.9	1300	6	ABA02496 Human G p
25	669	56.9	1312	4	AAH47911 Human G p
26	669	56.9	3689	8	ABZ42573 Human his
27	669	56.9	3689	12	ADO05719 Human his
28	669	56.9	3689	12	ADO29967 Human GPC
29	668	56.8	1170	9	AAI55126 Human H4
30	616.8	52.4	1170	6	AAI70983 Guinea pi
31	494.6	42.1	1166	9	AAD55124 Human H4
32	422.2	35.9	1103	9	AAD55123 Human H4
33	288.4	22.8	1326	6	AAI37667 Human G-p
34	257.8	21.9	540	6	AAS98150 Human DNA
35	158.4	13.5	1239	2	AAH84570 G-protein
36	158.4	13.5	1239	3	AAH84570 G-protein
37	158.4	13.5	2700	2	AAH84571 G-protein
38	158.4	13.5	2700	3	AAH84571 G-protein
39	153	13.0	1311	9	AAI59979 Human H3
40	151.2	12.9	1203	9	AAI59985 Human H3
41	140.6	12.0	1338	12	ADP66834 Murine hi
42	140.6	12.0	18105	8	ABZ82337 Mouse his
43	140	11.9	1098	4	AAH47749 Human his
44	139	11.8	2483	12	ADO30256 Mouse GPC
45	138.4	11.8	1023	4	AAH26798 Human his

## ALIGNMENTS

### RESULT 1

AAI70982

ID AAI70982 standard; cDNA; 1176 BP.

XX

AC AAI70982;

XX

DT 18-MAR-2002 (first entry)

XX

DE Rat histamine H4 receptor cDNA.

XX

KW Histamine H4 receptor; rat; antiaesthetic; antiallergenic;

KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;

KW diagnosis; gene therapy; ss.

XX

OS Rattus rattus.

XX

PN WO200192485-A1.

XX

PD 06-DEC-2001.

XX

PF 22-FEB-2001; 2001WO-US005914.

XX

PR 31-MAY-2000; 2000US-0208260P.

XX

PA (ORTH ) ORTHO-MCNEIL PHARM INC.

XX

PI Lovenberg T, Liu C;

XX

WPI: 2002-114339/15.

XX

DR P-PSDB; AAM50566.

XX

PT New mammalian histamine H4 receptor proteins and polynucleotides encoding

XX

PT the proteins, useful in gene therapy for treating diseases where it is

XX

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX

PS Claim 4; Fig 5C; 92pp; English.

XX

CC The present sequence is that of a cDNA clone encoding a rat histamine

XX

CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA

XX

CC library. It shows 72.5% homology to the human H4 receptor coding region.

XX

CC The invention provides mammalian (human, mouse, rat and guinea pig)

XX

CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and

XX

CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in

CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;  
 Query Match 100.0%; Score 1176; DB 6; Length 1176;  
 Best Local Similarity 100.0%; Pred. No. 0;  
 Matches 1176; Conservative 0; Mismatches 0; Indels 0; Gaps 0;  
 Qy 1 ATGTGCGAGTCTAAGCGCAGTCTGCTTGGCACTGCTCAAGTCCCTTGGCATTT 60  
 Db 1 ATGTGCGAGTCTAAGCGCAGTCTGCTTGGCACTGCTCAAGTCCCTTGGCATTT 60  
 Qy 61 TTAATGTCCTGCTTGTCTTATACGATAGGCAATGCTGTGTCATTTAGCCCTTT 120  
 Db 61 TTAATGTCCTGCTTGTCTTATACGATAGGCAATGCTGTGTCATTTAGCCCTTT 120  
 Qy 121 GTACGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTCT 180  
 Db 121 GTACGACAGAAACCTTAGACATCGAAGTAATTTTCTTAATTTGGCTATTCT 180  
 Qy 181 GACTTCTTGGTGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG 240  
 Db 181 GACTTCTTGGTGTGTCATCTCCATTCCTCTGTACATCCCTCACAGCTGTTAACTGG 240  
 Qy 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATTAATGCTATCTTTGTGACAGCA 300  
 Db 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATTAATGCTATCTTTGTGACAGCA 300  
 Qy 301 TCCGTCTACAGTATGTCCTCATTAATGCTACGATCGATACAGTCCAGTTCAGACGCTGTG 360  
 Db 301 TCCGTCTACAGTATGTCCTCATTAATGCTACGATCGATACAGTCCAGTTCAGACGCTGTG 360  
 Qy 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAATGTTGGCTGTTGG 420  
 Db 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAATGTTGGCTGTTGG 420  
 Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTGGAAGAACAGC 480  
 Db 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTGGAAGAACAGC 480  
 Qy 481 ACCAACACAGAGGAGTGGAGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Db 481 ACCAACACAGAGGAGTGGAGCTGCTGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
 Qy 541 GCATTTCTTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 Db 541 GCATTTCTTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
 Qy 601 TGGAGCTGTGGAGCGTGGAGTCTGATAGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 Db 601 TGGAGCTGTGGAGCGTGGAGTCTGATAGTGGCTTCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 660  
 Qy 661 ACCTTCTTCCAGGGGACCTGGACCTCAGCGAGAACTGGTGGCTTGTAGGACAAAGTCTT 720  
 Db 661 ACCTTCTTCCAGGGGACCTGGACCTCAGCGAGAACTGGTGGCTTGTAGGACAAAGTCTT 720  
 Qy 721 CCTGGATTAAGGAACCGACCGCTCTCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT 780  
 Db 721 CCTGGATTAAGGAACCGACCGCTCTCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT 780  
 Qy 781 CTCCTGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGTTC 840  
 Db 781 CTCCTGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGTTC 840

Qy 841 TTCTGCGATCAGAAAGCCAGTCTTACCAGAGAGACACGTTGAGCTTCTCAGAGGC 900  
 Db 841 TTCTGCGATCAGAAAGCCAGTCTTACCAGAGAGACACGTTGAGCTTCTCAGAGGC 900  
 Qy 901 AGGAAGCTAGCCAGGTCGCTAGTCTCTCTGAGTCTTTTGGCCATTTGCTGGGCTCCG 960  
 Db 901 AGGAAGCTAGCCAGGTCGCTAGTCTCTCTGAGTCTTTTGGCCATTTGCTGGGCTCCG 960  
 Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGAGAGGAGCGCCCAATCGATT 1020  
 Db 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGAGAGGAGCGCCCAATCGATT 1020  
 Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGTTCACATTTCACTTATTAATCCCTTCTATAC 1080  
 Db 1021 TGGTACAGCATAGCTTTTGGCTACAGTGTTCACATTTCACTTATTAATCCCTTCTATAC 1080  
 Qy 1081 CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
 Db 1081 CCTTTGTGCCACAGAGCTTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
 Qy 1141 CCAGCACCCTTCACAGAGCCAGTCAGTATCTTCTTGA 1176  
 Db 1141 CCAGCACCCTTCACAGAGCCAGTCAGTATCTTCTTGA 1176  
 RESULT 2  
 AAI70981  
 ID AAI70981 standard; cDNA; 1176 BP.  
 XX  
 AC AAI70981;  
 XX  
 DT 18-MAR-2002 (first entry)  
 XX  
 DE Mouse histamine H4 receptor cDNA.  
 XX  
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiac; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; ss.  
 XX  
 OS Mus musculus.  
 XX  
 FN W0200192485-A1.  
 XX  
 PD 06-DEC-2001.  
 XX  
 PF 22-FEB-2001; 2001WO-US005914.  
 XX  
 PR 31-MAY-2000; 2000US-0208260P.  
 XX  
 PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
 XX  
 PI Lovenberg T, Liu C;  
 XX  
 DR WPI; 2002-114339/15.  
 DR P-PSDB; AAM50565.  
 XX  
 PT New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 PS Claim 4; Fig 5A; 92pp; English.  
 XX  
 CC The present sequence is that of a cDNA clone encoding a murine histamine  
 CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen  
 CC cDNA library. It shows 72.8% homology to the human H4 receptor coding  
 CC region. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying



modulators of the mammalian histamine H4 receptor. Such modulators may be useful for diagnosing, treating or preventing asthma, allergy, inflammation, cardiovascular and cerebrovascular disorders, non-insulin dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of the neuroendocrine system, stress and spasticity

Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

Query Match 81.5%; Score 958.4; DB 6; Length 1176;  
Best Local Similarity 88.4%; Pred. No. 2.9e-300;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

1 ATGTCGAGTCTAAGCGCAGTCTGCTTGGCCACTGACTGCTCAAGTCCCTTCGCAATT 60  
1 ATGTCGAGTCTAAGCAGTCTGAGCATCTTGGCCAGCAGTCTGCTTGGCAATT 60  
61 TTAATGTCCTTGGCTTGGCTATACGATAGCAATGCTGTGCTCAATTTAGCCCTT 120  
61 TTAATGTCCTTGGCTTGGCTATACGATAGCAATGCTGTGCTCAATTTAGCCCTT 120  
121 GTAGCAGACAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180  
121 GTGTCGAGACAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCT 180  
181 GACTTCTCGTGGTGTCTATCCATCTCTGTATCATCTCCACAGCTGTAACTGG 240  
181 GACTTCTCGTGGTGTCTATCCATCTCTGTATCATCTCCACAGCTGTAACTGG 240  
241 AATTTGGAAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTTGTGACAGCA 300  
241 AATTTGGAAGTGAATCTGATGTTTGGCTCATTACTGACTATCTTTTGTGACAGCA 300  
301 TCCGCTACAGTATGCTCTCATTAGTACGATACGATACGATACGATTTCAACGCTGT 360  
301 TCTGCTACAATATGCTCTCATTAGTACGATACGATACGATTTCAACGCTGT 360  
361 CGTTATAGACACAGCAGTGGCATCTGAAATTTGCTTCAATTTGGTGGCTGTGG 420  
361 TCTTATAGGCTCAACACAGTGGCATGATGATTTGCTCAATTTGGTGGCTGTGG 420  
421 ATACTGGCTTTTGGTCAATGGCCATGATTTCTGGCTTCGGATTTCTGGAAGACAGC 480  
421 ATACTGGCTTTTGGTCAATGGCCATGATTTCTGGCTTCGGATTTCTGGAAGACAGC 480  
481 ACCAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGTATCATCTCCGCAATTACA 540  
481 ACAGAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGTATCATCTCCGCAATTACA 540  
541 GCATCTTTGGAAATCTCTGCTCTCTGCTTCTCTGCTGCTTCTTCAAGTGTACAGATTAC 600  
541 ATGCTCTTTGGAAATCTCTGCTCTCTGCTTCTCTGCTGCTTCTTCAAGTGTACAGATTAC 600  
601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTCCCTAGCCAGCTGGATTCTGCT 660  
601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTCCCTAGCCAGCTGGATTCTCCTACT 660  
661 ACCTCTTCCAGGGCAGTCTGACACTCAGCAGAACTGGGTTGGCTTTGAGACAGTCTT 720  
661 ACCTCTTCCAGGTCTTCAAGACACTTACAGAGCTGGGTTGGCTTTGAGACAGTCTT 720  
721 CCTGATTAAAGGAACAGCGCTGCTTCTTCAATTCAGAAAGTCCACAGGAAAGAGCAGT 780  
721 CCTGATTAAAGGAACAGCGTCTCTCTCACTCAGAAAGTCTCTCAGAAAGAGAGCAGC 780  
781 CTCCTGGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGTTC 840  
781 ATCTGGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAGTGGTTC 840  
841 TTCTCCGATCAGAAAGCCAGTGTCTTCAACAGAGAGCAGTGGAGCTTCTCAGAGGC 900  
841 TTCTGGCATCGAAAGTGCAGCGTCTTCCCAAGAGGAGTACGAGAGCTCTCAGAGGC 900  
901 AGGAAGTAGCAGGTCGCTAGTCTCTCTGCTGCTTTTGGCAATTTGCTGGGCTCCG 960

901 AGGAAGTAGCAGGTCAGTCCATCTTCTGAGCGCTTTTGGCAATTTGCTGGGCTCCA 960  
961 TATTGCTGTTCACAAATTTGTTTCAACTTATTCGAGAGGAGCGCCCAAAATCGATT 1020  
961 TACTGTCTGTTCACAAATTTGTTTCAACTTATTCGAGAGGAGCGCCCAAAATCGGTG 1020  
1021 TGGTACAGCAGTCTTTTGGCTACAGTGGTTCAATTCACCTTATTAATCCCTTCTATAC 1080  
1021 TGGTACAGCAGTCTTTTGGCTACAGTGGTTCAATTCGTTTGTAAATCCCTTCTGTAC 1080  
1081 CCTTTGTGCCACAGCAGCTTTCCAGAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140  
1081 CCTTTGTGTACAGGCTTTCCAGAGGCTTTCTGGAAGATACCTTTGTGTGACAAAGCAA 1140  
1141 CCAGCAGCTTCCAGAGCCAGTCTAGTATCTTCTTGA 1176  
1141 CCAGCGCTGTCCAGAGACCAAGTCTAGTATCTTCTTGA 1176

RESULT 3  
ADO30257  
ID ADO30257 standard; cDNA; 1538 BP.  
XX ADO30257;  
AC ADO30257;  
XX 29-JUL-2004 (first entry)  
XX Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.  
G protein-coupled receptor; GPCR; drug screening; diagnosis;  
transgenic mouse; neurological disorder; adrenal gland disorder;  
colon disorder; intestinal disorder; cardiovascular disorder;  
muscular disorder; blood disorder; immune disorder; bone disorder;  
joint disorder; metabolic disorder; nutritive disorder; cancer;  
kidney disorder; liver disorder; lung disorder; breast disorder;  
ovary disorder; uterus disorder; prostate disorder; testis disorder;  
skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
cytostatic; antinflammatory; vasotropic; antidiarrhoeic; antiarrhythmic;  
CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
dermatological; antiulcer; antithyroid; antiallergic; anorectic;  
immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
murine; gene; ss.  
Mus musculus.  
WO2004040000-A2.  
XX 13-MAY-2004.  
XX 09-SEP-2003; 2003WO-US028226.  
XX 09-SEP-2002; 2002US-0409303P.  
XX 09-APR-2003; 2003US-0461329P.  
XX (PRIM-) PRIMAL INC.  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
XX Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
XX WPI; 2004-390329/36.  
XX P-PSDB; ADO29497.  
XX Novel mammalian G protein coupled receptors, useful for identifying  
XX compounds that modulates diagnosing and treating disease condition  
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina  
XX pectoris, Parkinson's disease.  
XX Claim 151; SEQ ID NO 1360; 542pp; English.  
XX The invention relates to human and mouse G protein-coupled receptors

(GPCRs) and nucleic acids encoding them. The invention also relates to sequences at least 90% identical to the GPCR proteins and nucleic acids of the invention; methods of treating, preventing or diagnosing diseases associated with GPCRs of the invention; methods of screening for compounds useful in the treatment of GPCR-related diseases; a transgenic mouse comprising a GPCR gene of the invention; a mouse comprising a mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived from the transgenic mice; kits comprising several mice, each of which has a mutation in a different GPCR gene of the invention; and kits comprising probes which hybridize to GPCR polynucleotides of the invention. The invention further discloses variants of the GPCR polypeptides and vectors comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may be used in the diagnosis, treatment or prevention of a wide variety of diseases including neurological disorders (e.g., Alzheimer's disease, depression, diabetic neuropathy, Parkinson's disease or schizophrenia); disorders of the adrenal gland; disorders of the colon or intestine (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or myocardial infarction); muscular disorders; blood disorders (e.g., anemia or leukemia); immune disorders (e.g., autoimmune disorders or AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g., obesity, enzyme deficiency-related diseases or vitamin deficiency-related diseases); and disorders of the kidney, liver, lung, breast, ovary, uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and thyroid (e.g., cancers). The present sequence represents a GPCR-encoding nucleic acid of the invention. Note: The full sequence data for this patent did not form part of the printed specification; those sequences not shown were obtained in electronic format directly from WIPO at [ftp.wipo.int/pub/published\\_pct\\_sequences](http://ftp.wipo.int/pub/published_pct_sequences).

Sequence 1538 BP; 357 A; 362 G; 340 G; 479 T; 0 U; 0 Other;

Query Match 81.5%; Score 958.4; DB 12; Length 1538;  
Best Local Similarity 88.4%; Pred. No. 3.4e-300;  
Matches 1040; Conservative 0; Mismatches 136; Indels 0; Gaps 0;

1 ATGTCGGAGCTAAGCGACCTGAGCTGCTGCGACCTGCTCAAGTCCCTCGCATTT 60  
61 ATGTCGGAGCTAAGCGACCTGAGCTGCTGCGACCTGCTCAAGTCCCTCGCATTT 120  
61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
121 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 180  
121 GTACACAGACAACTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180  
181 GTGGTGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 240  
181 GACTTCTTCTGGGTGTCATCTCCATTCCTGTCATACATCCCTCACAGCTGTTAACTGG 240  
241 GACTTCTGCTGGGTGTCATCTCCATTCCTGTCATACATCCCTCACAGCTGTTAACTGG 300  
241 AATTTGGAAGTGAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
301 AATTTGGAAGTGAATCTGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
301 TCCGCTCTACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 360  
361 TCTGCTCTACATGATGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
361 CGTTTATAGACAGACACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 420  
421 TCTTATAGGGCTCAACACCTGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
421 ATACTGGCTCTTCTGGTCAATGGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
481 ATACTGGCTCTTCTGGTCAATGGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
481 ACCAACACAGAGGAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 540  
541 ACGAACACAAAGGAGTGGAGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600

541 GCATTTCTGGAAATCTCTGCTCCCTGCTCTCTGCTGCTCTATTTTCAGTGACAGATTAC 600  
601 ATGCTCTTGGAAATCTCTGCTCCCTGCTCTCTGCTCTATTTTCAGTGACAGATTAC 660  
601 TGGAGCTCTGGAAGCGTGGAGTCTCTCAGTAGTGGCTTACGACACCTGCTGATTCATCGCT 660  
661 TGGAGCTCTGGAAGCGTGGAGTCTCTCAGTAGTGGCTTACGACACCTGCTGATTCATCGCT 720  
661 ACCTCTCAGGGGCGACTGGACACTCACGAGAACTGGGTGGCTGTAGGACAACTCTT 720  
721 ACCTCTCAGGTCTCTCAGGACACTTACACAGAGCTGGGTGGCTGTAGGACAACTCTT 780  
721 CTTGGATTAAAGGAAACAGCGCGCATCCCTTCAATTCAGAAAGTCCACGAGAAAGAGCAGT 780  
781 CTTGGATTAAAGGAAACAGCTGCTCTCTGCTCTCAGAAAGTCTCTGAGAAAGAGCAGC 840  
781 CTCTGCTGTCTTAAAGGACTCATGAGCGGTAGTATCATCCCTTCAAAGTGGGTTC 840  
841 ATCTGCTGTCTTAAAGGACTCATGAGCGGTAGTATCATCCCTTCAAAGTGGGTTC 900  
841 TTCTGCGGATCAGAAAGCCAGTCTTCCACAGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900  
901 TTCTGCGGATCAGAAAGTGGAGCTTCCGCAAGGAGTACGACAGAGCTTCTCAGAGGC 960  
901 AGGAAGCTAGCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960  
961 AGGAAGCTAGCCAGGTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1020  
961 TATTGCTGTCTCAATTTGTTTCACTTATTCGAGAGGAGCGCCCAATCGATT 1020  
1021 TACTGCTGTCTCAATTTGTTTCACTTATTCGAGAGGAGCGCCCAATCGATT 1080  
1021 TGGTACAGATAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1080  
1081 TGGTACAGATAGCTTGGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1140  
1081 CCTTTGGCCACAGACGTTTCCAGAGGCTTCTGGAAGATCTCTGCTGTGACAAAGCAA 1140  
1141 CCTTTGGTGTACAGGCGTTTCCAGAGGCTTCTGGAAGATCTCTGCTGTGACAAAGCAA 1200  
1141 CCAGCAGCTTTCACAGACCCAGTCTGATCTCTTTGA 1176  
1201 CCAGCAGCTGTACAGAAACAGTCTGATCTCTTTGA 1236

RESULT 4  
AAI67750  
ID AAI67750 standard; cDNA; 1173 BP.  
XX  
AC AAI67750;  
XX  
AC AAI67750;  
DT 27-FEB-2002 (first entry)  
XX  
DE Human histamine H4 receptor protein encoding cDNA.  
XX  
DE Histamine receptor; H4; antirheumatic; antiarthritic; immunosuppressive;  
KW antiasthmatic; antiallergic; neuroprotective; antidiabetic; human;  
KW cerebroprotective; cAMP modulator; gene therapy; ss.  
XX  
OS Homo sapiens.  
XX  
FH Key Location/Qualifiers  
FT 1..1173  
FT /\*cag= a  
FT /product= "histamine H4 receptor"  
XX  
XX WO200185786-A2.  
XX  
XX 15-NOV-2001.  
XX  
XX 04-MAY-2001; 2001WO-US014527.  
XX  
XX 05-MAY-2000; 2000US-0202151P.  
PR

```
PR 23-AUG-2000; 2000US-0227567P.
PR 13-NOV-2000; 2000US-0247855P.
PA (AMHP ) AMERICAN HOME PROD CORP.
XX Jones PG, Blatcher M, Wu S, Pausch MH;
XX WPI; 2002-049442/06.
DR P-PSDB; AAG66023.
XX
XX New histamine receptor, termed H4 useful for detecting H4 (ant)agonists
PT for treating transplanted organ rejection, asthma, allergy, multiple
PT sclerosis and rheumatoid arthritis.
XX
XX Claim 13; Fig 1; 66pp; English.
XX
XX The invention provides an isolated histamine receptor, H4, which binds
CC ligands comprising imidazole attached to amine by an alkyl chain. The H4
CC receptor can be expressed by standard recombinant methodology. Cells
CC expressing H4 receptor protein at a detectable level can suppress cyclic
CC adenosine monophosphate (cAMP) formation when contacted with the H4
CC receptor agonist. The H4 receptor and antibodies are used for identifying
CC H4 receptor modulators. Modulation of histamine H4 receptors is useful
CC for treating transplanted organ rejection, asthma, allergies and
CC autoimmune pathologies such as multiple sclerosis, type I diabetes,
CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor
CC protein and nucleic acids are useful targets to identify drugs that are
CC effective in treating disorders associated with histamine-regulated
CC processes. Identification and isolation of H4 receptor provides for
CC development of screening of molecules that interact with H4 receptors.
CC Genetic variants of H4 can be used to diagnose an H4 associated disease
CC as described above. The H4 receptor polynucleotide is useful to treat or
CC prevent a disorder associated with the function of H4 in peripheral blood
CC leukocytes. The present sequence represents a cDNA encoding the human
CC histamine H4 receptor protein
XX
XX Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;
XX
XX Query Match 57.0%; Score 670.6; DB 6; Length 1173;
XX Best Local Similarity 74.3%; Pred. No. 1.2e-206;
XX Matches 876; Conservative 0; Mismatches 294; Indels 9; Gaps 2;
XX
Qy 1 ATGTCGGAGTCTACGGCAGCTGAGTCTTGGTCACTGCTGCTCAAGTCCCTTGGCAATT 60
Db 1 ATGCCAGATCTAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATT 60
Qy 61 TTAATGTCCTGCTTCTTGTCTATACGATAGCAGTCTGCTGCTCAATTTAGCCCTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATAGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCCATCTCT 180
Qy 181 GACTTCTTCTGGGTGTCAATCTCAATTCCTCTGTACATCCCTCAACGCTGTTAACTGG 240
Db 181 GACTTCTTCTGGGTGTCAATCTCAATTCCTCTGTACATCCCTCAACGCTGTTCAATGG 240
Qy 241 AATTTTGAAGTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Db 241 GATTTTGAAGTGGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTG 300
Qy 301 TCCGCTACAGTATTTGCTCCTCATTTAGCTACGATCGATACAGTCTGCTGCTGCTGCTG 360
Db 301 TCTGTATATACATTTGCTCCTCATTTAGCTATGATCGATACCTGCTGCTGCTGCTGCTG 360
Qy 361 CGTTATAGACACAGCAGCTGGCAATCTGAAATTTGTTGCTCAAAATGCTGGCTGTTGG 420
Db 361 AGTTATAGAACTCAACATACCTGGGCTCTGAAGATTTGTTACTCTGATGCTGGCCGCTTGG 420
Qy 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATTTGGCTTGGATTTGGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTGGTCAATGGCCCAATGATTTGATTTCTAGTCTTGGAGGA---- 476
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Qy 481 ACCAACACAGAGAGTGCAGCCTGGCTTTTCTTACTGAGTGGTATCATCTCTGCCATTACA 540
Db 477 --TGAAGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTTGCCATCACA 534
Qy 541 GCATTTCTTGGAAATTCCTGCTCCCTGCTGCTTGGTGGTGTATTTTCAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGGAAATTCGATGCCAGTCACTCTAGTCTGCTTTATTTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTGGGAGTCTCAGTAGGTGCCCCTAGCCAGCTGGGATTCATCGCT 660
Db 595 TGGAGCCTGTGGAAGCGTGGTATCTCAGTAGGTGCCCAGCCATCTCTGGACTGACTGCT 654
Qy 661 ACCTCTTCCAGGGGCACCTGGGACACTCAGCGCAGAACTTGGGTTGGCTTGTAGGACAGTCTT 720
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTAGAGGTAGACTATCTTTCAAGGAGATCTCTT 714
Qy 721 CCTGTGTAAGGAACACAGCCGATCTCTTCATTCAGAAAGTCCACGAGGAAAGAGAGT 780
Db 715 TCTGCATCGACAGAAAGTTCTCTGCACTCTCTTCATTTAGAGAGACAGAGAGAAAGAGTAGT 774
Qy 781 CTCTCTGGTGTCTTAAAGGACTCAGATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTCC 840
Db 775 CTGATGTTTCTCAAGAACCAAGATGATAGCAATGCTTCCAAATGGGTTCC 834
Qy 841 TTCTGCCGATCAGAAAGCCAGTCTTCCACAGAGAGACAGCTGGAGCTTCTTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTTCACCAAAGGGAACATGTTGAACCTGCTCAGAGCC 894
Qy 901 AGGAAGTAGCCAGCTGCTAGCTGCTCTCTGAGTGTCTTTTGCATTTGCTGGGCTCG 960
Db 895 AGGAGATTTAGCAAGTCACTGGCCATTTCTCTTAGGGGTTTTTGTCTTTGCTGGGCTCCA 954
Qy 961 TATTGCTGTTTCACAATTTGTTTCTTCACTTATCGCAGGGGAGCGCCCAAAATCGATT 1020
Db 955 TATTCTGTTTCACAATTTGTTTCTTCACTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014
Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCAATTCATTTAATTCCTTTCTATAC 1080
Db 1015 TGGTATAGAAATTCATTTTGGCTTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGGCCACAGACGTTTCCAGAGCTTTTCCAGAGATCTCTGTGTACACAAAGCAA 1140
Db 1075 CCATTTGTCTCAAGCGCTTTCAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134
Qy 1141 CCAGCAGCTTC--ACAGACCCAGTCACTATCTTCTTCA 1176
Db 1135 CCTTACCATCAACACAGCTCGGTCACTATCTTCTTAA 1173
XX
XX RESULT 5
XX AAA46023
XX ID AAA46023 standard; cDNA; 1173 BP.
XX
XX AC AAA46023;
XX
XX DT 22-AUG-2000 (first entry)
XX
XX DE Human G protein coupled receptor hRUP7 encoding cDNA SEQ ID NO:13.
XX
XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;
XX identification; agonist; screening; therapeutic; pharmaceutical; mutant;
XX ss.
XX
XX OS Homo sapiens.
XX
XX PN WO200022131-A2.
XX
XX PD 20-APR-2000.
XX
XX PF -13-OCT-1999; 99WO-US024065.
XX
XX PR 13-OCT-1998; 98US-00170496.
```





Db 955 TATTCTCTGTTCAAAATGTCCTTTCTTATTTATTCCTCAGCAACAGGCTCTAAATCAGTT 1014  
 Qy 1021 TGGTACAGCATAGCCTTTTGGCTACAGTGGTTCAATTCACCTTATTAATCCCTTTCTATAC 1080  
 Db 1015 TGGTATAGAAATGCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCCCTTTTGTAT 1074  
 Qy 1081 CTTTGTGCCACAGACGTTTCCAGAGGCTTTTCGGAAGATACCTCTGTGTGACAAAGCAA 1140  
 Db 1075 CCATTGTGTCAAGCGCTTTCAAGAGCTTTCTTGAAATATTTTGTATATAAAGCAA 1134  
 Qy 1141 CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176  
 Db 1135 CCTCTACCATCACAAACAGTCGGTCAAGTATCTTCTTAA 1173

## RESULT 7

AAF83203

ID AAF83203 standard; cDNA; 1173 BP.

AC AAF83203;

DX 09-JUL-2001 (first entry)

DX Human GPCR-like polypeptide, PFI-013 encoding cDNA.

XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiaesthetic;  
 KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;  
 KW osteopathic; neuroprotective; nootropic; dermatologic; gynecological;  
 KW signal transduction; ss.

XX Homo sapiens.

XX Key Location/Qualifiers  
 FT CDS 1..1173

FT /\*tag= a  
 FT /product= "PFI-013"

XX BP1096009-A1.

XX 02-MAY-2001.

XX 24-OCT-2000; 2000EP-00309364.

XX 29-OCT-1999; 99GB-00025641.

XX 20-APR-2000; 2000GB-00009973.

XX (PFI2 ) PFIZER LTD.

XX (PFI2 ) PFIZER INC.

XX Peter B, O'reilly MA;

XX WPI; 2001-309854/33.

XX P-PSDB; AAB62445.

XX New G-protein coupled receptor-like polypeptide, polynucleotide for  
 PT screening drug candidates for treating diseases associated with signal  
 PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.

XX Claim 1; Page 43; 66pp; English.

XX This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor  
 CC (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be  
 CC expressed by standard recombinant methodology. Antibodies and modulators  
 CC of PFI-013 are useful in the manufacture of a medicament for treating  
 CC allergic disorder, including extrinsic asthma, immunological disorders,  
 CC such as intrinsic asthma, vasculitic granulomatous disease, interstitial  
 CC and other pulmonary disease, including chronic obstructive pulmonary  
 CC disease (COPD), infectious, inflammatory disease, such as inflammatory  
 CC bowel disease and neoplastic and myeloproliferative diseases. They are  
 CC also useful for treating obesity, diabetes, metabolic, neurological  
 CC diseases, psychotherapeutics, urogenital disease, reproduction and sexual  
 CC medicine, inflammation, cancer, tissue repair, dermatology, photoaging,  
 CC skin pigmentation, osteoporosis, cardiovascular, gastrointestinal

CC diseases, allergy and respiratory disease, sensory organ disorders, sleep  
 CC disorders and hair loss. The PFI-013 protein and nucleic acid are useful  
 CC in the diagnosis and treatment of the above conditions and also for  
 CC screening drug candidates for the treatment of diseases associated with  
 CC signal transduction. The antibodies are also useful for enrichment of  
 CC eosinophils from mammalian, especially human blood and for detecting the  
 CC protein in biological samples

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 56.9%; Score 669; DB 4; Length 1173;  
 Best Local Similarity 74.2%; Pred. No. 3.8e-206;  
 Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGAGCTCTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60  
 Db 1 ATGCCAGATATAATAGCACAAATTTATCTACTAGCACTCGTGTACTTTAGCAATTT 60  
 Qy 61 TTAATGTCCTGCTTGGCTTTTGTATAAAGATAGGCAATGCTGTGGTCATTTTAGCCCTTT 120  
 Db 61 TTTATGTCCTTAGTAGCTTTTGTATAATGCTAGGAAAGCTTTGGTCATTTTAGCTTTT 120  
 Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTCTT 180  
 Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 180  
 Qy 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTAGATCCCTCACACGCTGTGTAAC 240  
 Db 181 GACTTCTTCGTGGGTGTCATCTCCATTCCTCTGTAGATCCCTCACACGCTGTGTAAC 240  
 Qy 241 AATTTTGGAAAGTGAATCTGCTATGTTTGGCTCAATTAATGACTATCTTTTGTGCACAGCA 300  
 Db 241 GATTTTGGAAAGGAATCTGCTATTTTGGCTCAATTAATGACTATCTTTTGTATGACAGCA 300  
 Qy 301 TCCGTCTACAGTATTTGCTCTCATTTAGCTACGATCGATACCAGTCAGTTTCAAACGCTGTG 360  
 Db 301 TCTGTATATAACATTTGCTCTCATCGACTATGATCGATACCTGTGTCAGTCTCAATGCTGTG 360  
 Qy 361 CGTTATAGACACAGCACACTGGCATCTGAAAATTTGTTGCTCAAAATGGTGGCTTTGG 420  
 Db 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTGG 420  
 Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGATTTCTTGGAAACACAGC 480  
 Db 421 GTGCTGGCTTCTTAGTGAATGGCCCAATGATCTAGTTTTCAGAGTCTTGAAGA--- 476  
 Qy 481 ACCAACACAGAGGAGTCGGAGCTGGCTTTGTTACTAGTGGGTACATCTCGCCATACACA 540  
 Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAAATGGTACATCTTGCATCACA 534  
 Qy 541 GCATTTCTTGAATTTCCCTGCTCCCTGCTCTCTGGTGGTCTATTTCAGTGTACAGATTAC 600  
 Db 535 TCATTTCTTGAATTTCTGGATCCCGAGTCACTCTTAGTCGCTTATTTCAACATGAATTTAT 594  
 Qy 601 TGGAGCTGTGGAAAGCTGGAGTCTCAGTAGGTGCTCCTAGCCACCGCTGGATTTCATCGCT 660  
 Db 595 TGGAGCTGTGGAAAGCTGTGATCTCAGTAGGTGCCAAGCCATCTCTGGACTGCTGCT 654  
 Qy 661 ACCTTTCCAGGGGCACTGGACACTCACGGAGAACTGGTGGTGTGTAGACAAAGTCTT 720  
 Db 655 GTCTTCTTCAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
 Qy 721 CCTGGATTAAAGGAACACAGCGGATCCCTTCATTCAGAAAGTCCACGAGGAAGAGCAGT 780  
 Db 715 TCTGCATTCGACAGAAAGTTCCTGCACTCTTCATTCAGAGAGACAGAGAGAAAGAGTAGT 774  
 Qy 781 CTCCTGTGTCTTTAAGGACTCACATGAGGGGTAGTATCATCGCTTCTCAAAGTGGTTC 840  
 Db 775 CTGATGTTTCTTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGTTC 834  
 Qy 841 TTCTGCCGATCAGAAAGCCCGCTCTCACAGAGAGACAGCTGGAGCTCTCTCAGAGGC 900  
 Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACCTGCTTTAGAGCC 894





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Db 361 TCCTATAGAACTCAACATCTGGGCTCTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATCTCGCTCGGATTTCTGGAAAGAACAGC 480
Db 421 GTGCTGGCTTTCTTGGTCAATGGCCCAATGATCTCGCTCGGATTTCTGGAAAGAACAGC 476
Qy 481 ACCAACACAGAGGAGTGGGAGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTTACA 540
Db 477 -TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 534
Qy 541 GCATTTCTTGAATTTCTCTGCTCCCTGCTCTCTGCTGCTCTGCTCTGCTCTGCTCTGCT 600
Db 535 TCATTTCTTGAATTTCTGCTCCCTGCTCTCTGCTCTGCTCTGCTCTGCTCTGCTCTGCT 594
Qy 601 TGGAGCTGTGGAGCTGGAGGCTCTCAGTAGTGGTCCCTAGCCACGCTGGATTCATCGCT 660
Db 595 TGGAGCTGTGGAGCTGGAGGCTCTCAGTAGTGGTCCCTAGCCACGCTGGAGCTGACTGCT 654
Qy 661 ACCTCTCCAGGGCACTGGACACTCAGCAGACTGGTGGTGGTGGTGGTGGTGGTGGTGGT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTAAAGGAACAGCGGCTCTCTCTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780
Db 715 TCTGCATCGACAGAGTCTCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 774
Qy 781 CTCTGTGTCTTAAAGACTCAATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTTC 840
Db 775 CTATGTCTTCTCAAGAACCAAGATGAATAGCAATACAATTTGCTTCCAAATGGGTTC 834
Qy 841 TTCTGCCATCAGAAAGCCAGTCTTCCAGAGAGAGCAGCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCAAAGGGAACATGTTGAAGCTCTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGTCTGCTGCTCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 960
Db 895 AGGATATTAGCAAGTCACTGGCCATCTCTGAGGGTCTTGTGCTGCTGCTGCTGCTGCT 954
Qy 961 TATTGCTGTTCACAAATGTTTTCACACTTATCGCAGAGGGGAGCGCCCAATCGATT 1020
Db 955 TATTCTGTTCACAAATGTTTTCACACTTATTCCTCAGCAACAGGCTCTTAATCAGTT 1014
Qy 1021 TGGTACAGCTAGCTTTTGGCTACAGTGGTTCATTCACCTTATTAATCTCTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAAGTGGTTCATTCCTTGTCAATCTCTTGTAT 1074
Qy 1081 CTTTGTGCCACAGACGTTTCCAGAGGCTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTCTTGAATAATTTTGTATAAAAGCAA 1134
Qy 1141 CCAGCAGCTTC---ACAGACCACTGATGATCTTCTTGA 1176
Db 1135 CCTACCATCACAAACAGTCGGTCACTATCTTCTTAA 1173
```

## RESULT 9

ABZ80663

ID ABZ80663 standard; cDNA; 1173 BP.

XX AC

AC ABZ80663;

XX AC

DT 13-JUN-2003 (first entry)

XX AC

XX Human histamine receptor coding sequence.

XX KW

human, histamine receptor; gene; ds; chromosome 18; anti-inflammatory;  
anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;  
anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;  
neuroprotective; inflammation; asthma; allergy; atopic dermatitis;  
myocardial infarction; migraine; chronic obstructive pulmonary disease;  
rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;  
psoriasis; receptor.





```
QY 241 AATTTTGGAAAGTGAATCTGCTGTTTGGCTCAATTAAGTCTATCTTTGTGCACAGCA 300
Db 241 GATTTTGGAAAGGAATCTGCTGTTTGGCTCAATTAAGTCTATCTTTGTGCACAGCA 300
QY 301 TCCGCTACAGTATGTCCTCATTAGTACGATACGATACGATACGATACGATACGATACGAT 360
Db 301 TCTGTATATAACATGTCCTCATCAGCTATGATCGATACGATACGATACGATACGATACGAT 360
QY 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAATTTGTTGCTGTTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTTGAAGATTGTTTACTCTGATGGTGGCGTTTGG 420
QY 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGATTCCTGGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGATTCCTGGAAGAACAGC 476
QY 481 ACCAACACAGAGGAGTGGAGCCCTGGCTTTGTTACTGAGTGGTACATCTCTCGCATPACA 540
Db 477 -TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTCGCATPACA 534
QY 541 GCATCTTGGAAATCTCTGCTCCCTGCTCTCTGTTGGTCTATTTCAAGTGTACGATTTAC 600
Db 535 TCATCTTGGAAATCTCTGCTCCCTGCTCTCTGTTGGTCTATTTCAAGTGTACGATTTAT 594
QY 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTACGACGCTGATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTACGACGCTGATTCATCGCT 654
QY 661 ACCTCTTCCAGGGGCACTGACACTCACGAGAACTGGTGGCTTTAGGACAAAGTCTT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
QY 721 CTTGGATTAAGGAACAGCGGCTCTCTTCAATCAGAAAGTCCACAGGAAAGAGCAGT 780
Db 715 TCTGCACTGACAGAGTCTCTGCTCTCTTCAATCAGAGAGACAGAGAGAGAGTAGT 774
QY 781 CTCTGCTGCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTCC 840
Db 775 CTATGTTTCTTCAAGAACGAGTGAATAGCATACATTTGTTTCAAAATGGGTCC 834
QY 841 TTTCTGCGATCAGAAAGCCAGTGTCTTCCAGAGAGACAGCGTGGAGCTTCTCAGAGGC 900
Db 835 TTTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATGTTGAAGCTCTTAGAGCC 894
QY 901 AGGAGCTAGCGAGTCTGCTGCTCTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTG 960
Db 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTG 954
QY 961 TATTGCTGTTCAAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020
Db 955 TATTCTCTGTTCAAAATGTTCTTCAACTTATTTCTTCTCAGCAGCAGGCTCTTAATCAGTT 1014
QY 1021 TGGTACAGCATAGCTTTTGGCTACAGTGTTCATTTCACTTATTAATTCCTTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
QY 1081 CCTTTGGCCACAGACGTTTCCAGAGCGTCTTCTGGAAGATCTCTGTCGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGAGCGCTTTCAAAGGCTTCTTGAAGAAATATTTTGTATAAAAAGCAA 1134
QY 1141 CCAGCAGCTTC---ACAGAGCCAGTCAAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACACAGCTGGTCAAGTATCTTCTTAA 1173
```

## RESULT 11

AAI70980

ID AAI70980 standard; cDNA; 1173 BP.

XX

AC AAI70980;

XX

DT 18-MAR-2002 (first entry)

XX

```
DE Human histamine H4 receptor cDNA.
XX
KW Histamine H4 receptor; human; antiasthmatic; antiallergenic;
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;
XX diagnosis; gene therapy; ss.
OS Homo sapiens.
XX
PN W0200192485-A1.
XX
PD 06-DEC-2001.
XX
PF 22-FEB-2001; 2001WO-US005914.
XX
PR 31-MAY-2000; 2000US-0208260P.
XX
(ORTH ) ORTHO-MCNEIL PHARM INC.
XX
Lovenberg T, Liu C;
XX
WPI; 2002-114339/15.
DR P-PSDB; AAM50564.
XX
New mammalian histamine H4 receptor proteins and polynucleotides encoding
PT the proteins, useful in gene therapy for treating diseases where it is
PT beneficial to elevate mammalian histamine H4 receptor activity.
XX
PS Claim 4; Fig 1; 92pp; English.
XX
The present sequence is that of cDNA clone pH4R encoding a human
CC histamine receptor of the H4 subtype. The cDNA was isolated from a bone
CC marrow cDNA library. The invention provides mammalian (human, mouse, rat
CC and guinea pig) histamine H4 receptor nucleic acid molecules (see
CC AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have
CC been expressed in recombinant host cells that produce active recombinant
CC protein. The pharmacology of known histamine ligands is demonstrated.
CC Mammalian histamine H4 receptor may be used in gene therapy for the
CC treatment of diseases where it is beneficial to elevate mammalian
CC histamine H4 receptor activity. Recombinant protein is useful for
CC identifying modulators of the human histamine H4 receptor. Such
CC modulators may be useful for diagnosing, treating or preventing asthma,
CC allergy, inflammation, cardiovascular and cerebrovascular disorders, non-
CC insulin dependent diabetes mellitus, hyperglycemia, constipation,
CC arrhythmia, disorders of the neuroendocrine system, stress and spasticity
XX
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
Query Match 56.9%; Score 669; DB 6; Length 1173;
Best Local Similarity 74.2%; Pred. No. 3.8e-206;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
QY 1 ATGTCGGAGTCTAACGGCACTGAGCTTGGCACTGCTGCTCAAGTCCCTTGGCAATTT 60
Db 1 ATGCCAGATATAATAGACACAATCAATTTATCACTAGCACTGCTGTACTTTAGCATTT 60
QY 61 TTAATGTCCTGCTTGGCTTTTGTCTATAACGATAGGCAATCTGTGGTCATTTTAGCCTTT 120
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCATTTTAGCCTTT 120
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTTTCTTAATTTTGGCTATTCTTCT 180
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTTGGCCATCTCT 180
QY 181 GACTTCTTCTGGGTGTCATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTAACTGG 240
Db 181 GACTTCTTCTGGGTGTCATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTAACTGG 240
QY 241 AATTTTGGAAAGTGAATCTGATGTTTGGCTCAATTAAGTCTATCTTTGTGCACAGCA 300
Db 241 GATTTTGGAAAGGAATCTGCTGTTTGGCTCAATTAAGTCTATCTTTGTGCACAGCA 300
QY 301 TCCGCTACAGTATGTCCTCATTAGTACGATACGATACGATACGATACGATACGATACGAT 360
Db 301 TCTGTATATAACATGTCCTCATCAGCTATGATCGATACGATACGATACGATACGATACGAT 360
QY 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAATTTGTTGCTGTTGTTGG 420
Db 361 TCTTATAGAACTCAACATACCTGGGCTTGAAGATTGTTTACTCTGATGGTGGCGTTTGG 420
QY 421 ATACTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGATTCCTGGAAGAACAGC 480
Db 421 GTGCTGGCTTCTTGGTCAATGGCCCAATGATCTGGCTTCGATTCCTGGAAGAACAGC 476
QY 481 ACCAACACAGAGGAGTGGAGCCCTGGCTTTGTTACTGAGTGGTACATCTCTCGCATPACA 540
Db 477 -TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTCTCGCATPACA 534
QY 541 GCATCTTGGAAATCTCTGCTCCCTGCTCTCTGTTGGTCTATTTCAAGTGTACGATTTAC 600
Db 535 TCATCTTGGAAATCTCTGCTCCCTGCTCTCTGTTGGTCTATTTCAAGTGTACGATTTAT 594
QY 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTACGACGCTGATTCATCGCT 660
Db 595 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTACGACGCTGATTCATCGCT 654
QY 661 ACCTCTTCCAGGGGCACTGACACTCACGAGAACTGGTGGCTTTAGGACAAAGTCTT 720
Db 655 GTCTCTTCCAACTCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 714
QY 721 CTTGGATTAAGGAACAGCGGCTCTCTTCAATCAGAAAGTCCACAGGAAAGAGCAGT 780
Db 715 TCTGCACTGACAGAGTCTCTGCTCTCTTCAATCAGAGAGACAGAGAGAGAGTAGT 774
QY 781 CTCTGCTGCTTAAAGGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGGTCC 840
Db 775 CTATGTTTCTTCAAGAACGAGTGAATAGCATACATTTGTTTCAAAATGGGTCC 834
QY 841 TTTCTGCGATCAGAAAGCCAGTGTCTTCCAGAGAGACAGCGTGGAGCTTCTCAGAGGC 900
Db 835 TTTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATGTTGAAGCTCTTAGAGCC 894
QY 901 AGGAGCTAGCGAGTCTGCTGCTCTCTGCTGCTTCTGCTGCTTCTGCTGCTGCTGCTG 960
Db 895 AGGAGATTAGCCAGTCACTGGCCATCTCTTGGGGTCTTCTGCTGCTGCTGCTGCTGCTG 954
QY 961 TATTGCTGTTCAAAATGTTCTTCAACTTATCGCAGAGGGAGCGCCCAAAATCGATT 1020
Db 955 TATTCTCTGTTCAAAATGTTCTTCAACTTATTTCTTCTCAGCAGCAGGCTCTTAATCAGTT 1014
QY 1021 TGGTACAGCATAGCTTTTGGCTACAGTGTTCATTTCACTTATTAATTCCTTTCTATAC 1080
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
QY 1081 CCTTTGGCCACAGACGTTTCCAGAGCGTCTTCTGGAAGATCTCTGTCGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGAGCGCTTTCAAAGGCTTCTTGAAGAAATATTTTGTATAAAAAGCAA 1134
QY 1141 CCAGCAGCTTC---ACAGAGCCAGTCAAGTATCTTCTTGA 1176
Db 1135 CCTTACCATCACACAGCTGGTCAAGTATCTTCTTAA 1173
```

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Db 301 TCTGTATATAACATTGTCTCATCAGCTATGATCGATACCTGTGTCAGTCTCAAAATGCTGTG 360
Qy 361 CGTTATAGACACACACACTGGCATCTGAAATTTGTGCTCAAAATGCTGTGTTGG 420
Db 361 TCTTATAGAACTCAACATCTGGGCTCTGAAGATTTGTTACTCTGATGGTGGCCGTTTGG 420
Qy 421 ATACTGGCTTTCTTGGTCAATGGCCCATGATCTGGCTTCGGATTTCTTGGAGAACACAGC 480
Db 421 GTGCTGGCTTCTTGTAGTGAATGGGCAATGATTTCTAGTTTCAGAGTCTTGGAAAGGA---- 476
Qy 481 ACCAACACAGAGGAGTGGAGCCTGGCTTGTACTGAGTGGTATACATCTCGCCATTTACA 540
Db 477 --TGAGGTAGTGAATGGGCAATGATTTTTCGGAAATGGTATACATCTTGGCCATCACA 534
Qy 541 GCATTTCTTGAATCTCTGCTCCCTGCTCTCTTGGTGGTCTATTTCAAGTGTACAGATTTAC 600
Db 535 TCATTTCTTGAATTCGTGATCCCATCTATCTTAGTCGCTTATTTTCAACATGAATATTTAT 594
Qy 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTAGCCAGCTGGATTTATCGCT 660
Db 595 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGTGGCTTAGCCAGCTGGATTTATCGCT 654
Qy 661 ACCTCTTCCAGGGGCACTGGACACTCAGCGAGAACTGGGTTGGCTTGTAGGACAAAGTCTT 720
Db 655 GTCTCTTCCACATCTGTGGACATCTATTAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 721 CCTGGATTTAAAGAACCGCCGCTCTCTTCAATTCAGAAAGTCCACGAGGAAAGAGCAGT 780
Db 715 TCTGCATCGACAGAAAGTTCTCTGCATCTCTTCAATTCAGAGACAGACAGAGAGAGTAGT 774
Qy 781 CTCTGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGTTC 840
Db 775 CTCTGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAAAAGTGGTTC 834
Qy 841 TTCTGCCGATCAGAAAGCCAGTCTTCCACAGAGAGACAGCTGGAGCTTCTCAGAGGC 900
Db 835 TTCTCCCATCAGATCTGTAGTCTTCCACCAAGGAAACATGTTGAATCTCTTAGAGCC 894
Qy 901 AGGAAGCTAGCCAGTCTGCTGCTCTGAGTGTCTTGTGCAATTTGCTGGGCTCG 960
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTGTGTTGCTGGGCTCA 954
Qy 961 TATTGCTGTTCACAAATGTTCTTCAACTTATCGCAGAGGGGAGCGCCCAATTCGAT 1020
Db 955 TATTCTGTGTACAAATGTTCTTCAATTTATTTCTCAGCAACAGGTCCTTAAATCAGTT 1014
Qy 1021 TGGTACAGATAGCTTTTGGCTACAGTGTCAATTCACATTTATTAATCCCTTCTATAC 1080
Db 1015 TGGTATGAATGCAATTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074
Qy 1081 CCTTTGTGCCACAGACGTTTCCAGAAGGCTTTCTGGAAGATACCTGTGTGACAAAGCAA 1140
Db 1075 CCATTGTGTCAAGCGCTTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAGCAA 1134
Qy 1141 CCAGACCTTC---ACAGACCCAGTCAATCTCTCTTGA 1176
Db 1135 CCTTACCATCACAAACACAGTCGGTCAATCTCTCTTAA 1173
```

## RESULT 12

ACA93262

ID ACA93262 standard; cDNA; 1173 BP.

XX

AC ACA93262;

XX

DT 16-JUL-2003 (first entry)

XX

DE Human cDNA encoding GPCR hrUP7.

XX

Human; ss; gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
hARE-5; hrUP3; hrUP5; hrUP6; hrUP7; hGPCR27; hARE-1; hARE-2; hrPR1; hG2A;  
hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hrUP4; signalling cascade.

XX

OS Homo sapiens.  
XX US2003017528-A1.  
XX 23-JAN-2003.  
XX  
XX 06-JUN-2001; 2001US-00875076.  
XX  
XX 20-NOV-1998; 98US-0109213P.  
PR 16-FEB-1999; 99US-0120416P.  
PR 26-FEB-1999; 99US-0121852P.  
PR 12-MAR-1999; 99US-0123946P.  
PR 12-MAR-1999; 99US-0123949P.  
PR 28-MAY-1999; 99US-0136436P.  
PR 28-MAY-1999; 99US-0136437P.  
PR 28-MAY-1999; 99US-0136439P.  
PR 28-MAY-1999; 99US-0136567P.  
PR 28-MAY-1999; 99US-0137127P.  
PR 28-MAY-1999; 99US-0137131P.  
PR 29-JUN-1999; 99US-0141448P.  
PR 29-SEP-1999; 99US-0156333P.  
PR 29-SEP-1999; 99US-0156555P.  
PR 29-SEP-1999; 99US-0156634P.  
PR 12-OCT-1999; 99US-00417044.  
XX

(CHEN/) CHEN R.  
(DANG/) DANG H T.  
(LIAN/) LIAN C W.  
(LINI/) LIN I.

Chen R, Dang HT, Lian CW, Lin I;

WPI; 2003-428952/40.

P-PSDB; ABU92265.

Novel endogenous, orphan, human G protein-coupled receptors useful for identification of modulators of the receptor and as research tools for understanding the role of the receptor in human body.

Claim 25; Page 22; 54pp; English.

The invention relates to a human G protein-coupled receptor (GPCR) appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named hARE-3, hARE-4, hARE-5, hrUP3, hrUP6, hrUP7, hGPCR27, hARE-1, hARE-2, hrPR1, hG2A, hCHN3, hCHN4, hCHN6, hCHN8, hCHN9, hCHN10 and hrUP4. Also included are a plasmid comprising a vector and one of the cDNAs above and a host cell comprising the plasmid. The GPCRs are useful for the direct identification of candidate compounds as inverse agonists, agonists or partial agonists. In vitro and in vivo systems incorporating GPCRs is useful for elucidating and understanding the roles these receptors play in the human condition, both normal and diseased, as well as understanding the role of constitutive activation as it applies to understanding the signalling cascade. The cDNAs are useful for making a probe for dot-blot analysis against tissue mRNA and/or RT-PCR identification of the expression of the receptor in tissue samples. The present sequence is a cDNA encoding a GPCR of the invention

SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 56.9%; Score 669; DB 8; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 3.8e-206;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCAGCTGCTTGGCAGTCTGCTCAAGTCCCTTGGCATTT 60  
|||  
Db 1 ATGCCAGATCTAATAGCACAAATCAATTTATCATTAGCACTCTGTGTACTTTAGCATTT 60  
|||  
Qy 61 TTAATGTCCTGCTGCTTTTGTCTATAACGATAGCAATGCTGTGGTCAATTTAGCCTTT 120  
|||  
Db 61 TTTATGTCCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTT 120  
|||  
Qy 121 GTACACACAGAAACCTTAGCATCTGGAAGTAAATTTTCTTAATTTGGCTATTCT 180  
|||



Db 1 ATGCAGATCTAATAGACAAATCAATTTATCATCTAGCACTCGTGTCTTATAGCATTT 60  
Qy 61 TTAATGTCCTGCTGCTTTGCTATACGATAGCAATGCTGTGGTCATTTTAGCCTTT 120  
Db 61 TTTATGCTCTTAGTAGCTTTTGCTATATATGCTAGGAATGCTTTGGTCATTTAGCTTT 120  
Qy 121 GTAGCAGACAAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180  
Db 121 GTGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAATTTGGCTATTTCT 180  
Qy 181 GACTTCTTGTGGGTGCTCATCTCCATTCTCTGTACATCCCTCACAGCGCTGTTAACTGG 240  
Db 181 GACTTCTTGTGGGTGCTCATCTCCATTCTCTGTGTACATCCCTCACAGCGCTGTTGAATGG 240  
Qy 241 AATTTGGAAGTGAATCTGCATGCTTTGGCTCAATTAAGTACTATCTTTTGTGCACAGCA 300  
Db 241 GATTTGGAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGACAGCA 300  
Qy 301 TCCGTCTACATGATTTGCTCTATAGTACATCGATCAGTACAGTTCAGTTCAACGCTGTG 360  
Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGAGTCTCAATGCTGTG 360  
Qy 361 CGTTATAGCAGACACACTGGCATCTGAAATTTGTTGCTCAAAATGCTGGCTGTTGG 420  
Db 361 TCTTATAGAACTCAACATAGTGGGTCTTGAAGATTGTTACTGTAGTGGTGGCTGTTGG 420  
Qy 421 ATACTGGCTTTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGAAGAAGCAGC 480  
Db 421 GTGCTGGCTTTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGTCTTGAAGGA--- 476  
Qy 481 ACCAACACAGAGGAGTGGAGCGCTGGCTTTGTTACTGAGTGGTACATCTCGCCATTTACA 540  
Db 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534  
Qy 541 GCATTTCTGGAATTCCTCCCTGCTCCTGTTGCTGCTATTTTTCAGTGTACAGATTAC 600  
Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCACTTTAGTGGCTTATTTTCAACATGAATTTAT 594  
Qy 601 TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCTTCAGTCCGCTGGATTCATCGCT 660  
Db 595 TGGAGCTGTGGAAGCGTGATCACTCAGTAGGTGCTTCAGTCCGCTGGAGTCTGCT 654  
Qy 661 ACCTTCTCAGGGGCACTGGAACATCTACGCGAAGTGGGTGGTGTAGGACAGTCTT 720  
Db 655 GTCTCTTCCAACTCTGTGGACACTCAATTCAGAGGTAGACTATCTTCAAGAGAGATCTTT 714  
Qy 721 CCTGGATTAAAGGAACAGCGCATCCCTTCAATTCAGAAAGTCCACGAGGAAGAGCAGT 780  
Db 715 TCTGATCGACAGAGTTTCTGATCTCTTTCATTCAGAGAGACAGAGAGAGAGTAGT 774  
Qy 781 CTCCTGTGTCTTAAAGACTCACATGAGCGGTAGTATCATCGCTTCAGAGTGGGTTC 840  
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCAGAAATGGGTTC 834  
Qy 841 TTCTGCCATCAGAAAGCCCAAGTGTTCACAGAGAGACAGCGTGGAGCTTCTCAGAGGC 900  
Db 835 TTCTCCCAATCAGATTTCTGTAGCTTTCACCAAGGGAACATGTTGAAGTCTGTAGAGCC 894  
Qy 901 AGGAAGCTAGCCAGTCTGCTGCTCTCTGAGTGTCTTTGCAATTTGCTGGGCTCG 960  
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTGTGTTGCTGGGCTCCA 954  
Qy 961 TATTGCTGTTTCACAATGTTCTTCACTTATCCAGAGGGAGCGGCCCAATTCGATT 1020  
Db 955 TATTCTGTTTCACAATGTTCTTCACTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014  
Qy 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCAATTCATTTAAATCCCTTCTATAC 1080  
Db 1015 TGGTATAGAAATGCAATTTTGGCTTCAAGTGGTTCATTTCTTGTCAATCTCTTTGTAT 1074  
Qy 1081 CCTTTGTCACAGAGCTTTCAGAGGCTTCTGGAAGATCTCTGTGTACAAAGCAA 1140  
Db 1075 CCATTTGTGTCAAGCGCTTTTCAAGAGGCTTTCTTGAAGAAATATTTTGTATAAAAAGCAA 1134

Qy 1141 CCACACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176  
Db 1135 CCTCTACCATCACAAACACAGTCGGTCAGTATCTTCTTAA 1173

## RESULT 14

ABS57063

ID ABS57063 standard; cDNA; 1173 BP.

XX ABS57063;

XX 28-JAN-2003 (first entry)

XX Human cDNA encoding G-protein coupled receptor AXOR35.

Human; ss; gene: G-protein coupled receptor; AXOR35; lymphocyte; macrophage; eosinophil; neutrophil; infection; transplant rejection; gastrointestinal disorder; gastric ulcer; inflammatory bowel disease; Crohn's disease; irritable bowel syndrome; vomiting; inflammation; atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis; psoriasis; urological disease; urinary retention; cardiovascular disease; myocardial infarction; hypotension; hypertension; pulmonary disorder; chronic obstructive pulmonary disease; cough; renal disease; renal ischaemia; arteriosclerosis; atherosclerosis; psychosis; neurological disorder; migraine; anorexia; anxiety; schizophrenia; dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock; graft versus host disease; osteoporosis.

XX Homo sapiens.

XX Key Location/Qualifiers

FH CDS 1..1173

FT /\*tag= a

FT /product= "AXOR35"

XX US2002137054-A1.

XX 26-SEP-2002.

XX 20-JUL-2001; 2001US-00910411.

XX 02-NOV-1999; 99US-00431898.

XX 03-FEB-2000; 2000US-00497790.

XX 20-OCT-2000; 2000US-00693761.

XX (SMIK ) SMITHKLINE BEECHAM CORP.

XX (SMIK ) SMITHKLINE BEECHAM PLC.

XX Aubart KM, Bergsma DJ, Fitzgerald L, Graybill TL, Li X;

XX Michalovich D, Morrow DM, Zhu Y;

XX WPI: 2003-074982/07.

XX P-PSDB; ABG71960.

Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for treating infections, gastrointestinal disorders, autoimmune disorders, urological diseases, cardiovascular diseases and cancer.

XX Claim 2; Page 21-22; 24pp; English.

The invention relates to an isolated G-protein coupled receptor polypeptide, AXOR35, (and its homologues and variants) and its encoding polynucleotide (and its homologues, variants, complements and RNA equivalents). Also included are an anti-AXOR35 antibody, an AXOR35 expression vector, producing a recombinant host cell by introducing the vector into a cell such that the host cell produces AXOR35, a membrane of the host cell expressing AXOR35, identifying/screening for agonists or antagonists of AXOR35 and inhibiting or promoting the function of lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue, by administering to the patient AXOR35 agonists or antagonists. The agonist or antagonist identified is useful for treating a disease such as asthma, or for inhibiting or promoting the function of lymphocytes.

macrophages, eosinophils, or neutrophils in diseased tissue such as an  
aerobic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
for identifying compounds that are agonists or antagonists of AXOR35, as  
vaccines, or for treating infections (bacterial, fungal, protozoan or  
viral infections), transplant rejection, gastrointestinal disorders (such  
as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
irritable bowel syndrome, vomiting, inflammation (such as atopic  
dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
psoriasis), neurological diseases (such as urinary retention),  
cardiovascular diseases (such as myocardial infarction), hypotension,  
hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
disease), cough, renal diseases (such as renal ischaemia),  
arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
(such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
versus host disease and osteoporosis. The present sequence is the cDNA  
encoding AXOR35

XX  
SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Query Match 56.98; Score 669; DB 10; Length 1173;  
Best Local Similarity 74.21; Pred. No. 3.8e-206;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAAGCGCACTGCTGTCACACTGCTGCTCAAGTCCCTTGGCATTT 60  
DB 1 ATGCCAGATCTAATAGCAACAATTTATCTAGCACTCGTGTACTTTAGCATTT 60  
QY 61 TTAATGTCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
DB 61 TTTATGTCCTTAGTAGCTTTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 120  
QY 121 GTAGCAGACGAACCTTACACATCGAAGTAATTTTCTTAATTTGGCTATTTCT 180  
DB 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTTGGCCATCTCT 180  
QY 181 GACTTCTTCCTGGGTGTCTATCTCCATCTCTGTACATCCCTCACAGCTGTTTAACTGG 240  
DB 181 GACTTCTTCCTGGGTGTCTATCTCCATCTCTGTACATCCCTCACAGCTGTTTAACTGG 240  
QY 241 AATTTTGGAAAGTGTGATCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 300  
DB 241 GATTTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
QY 301 TCCGCTCTACAGTATGTCCTCATTAGCTAGCTAGCTAGCTAGCTAGCTAGCTAGCT 360  
DB 301 TCTGTATTAACATTTGTCCTCATCAGCTATGATGATGATGATGATGATGATGATGAT 360  
QY 361 CGTTATAGACACAGCACACTGGCATCTCGAAATTTGCTCAAAATGGTGGCTGTTTGG 420  
DB 361 TCTTATAGACTCAACATCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTTGG 420  
QY 421 ATACTGCTTTCTTGGTCAATGGCCCAATGATCTGCTGCTGCTGCTGCTGCTGCTGCT 480  
DB 421 GTGCTGGCCCTCTTAGTGAATGGGCCAATGATTTCTAGTTTCTAGAGTCTTGGAGGA--- 476  
QY 481 ACCAACACAGAGGAGTCGGAGCTGGCTTGTACTGAGTGGTATCATCTCGCCATTACA 540  
DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTATCATCTTGGCCATACA 534  
QY 541 GCATTTCTTGAATTTCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600  
DB 535 TCATTTCTTGAATTTCTGATCCCAAGTCTATCTTAGTCTGCTTATTTCAACATGAATTTAT 594  
QY 601 TGGAGCCTGTGGAAGCGTGGAGGCTCTCAGTAGGTGCTTACGCCACGCTGGATTCATCGCT 660  
DB 595 TGGAGCCTGTGGAAGCGTGTATCTCAGTAGGTGCTTACGCCACGCTTCTGGAAGTCTGCT 654  
QY 661 ACCTCTTCCAGGGGCACTGGACACTCAGCAGACTCGGTGGCTTGTAGGACAAAGTCTT 720  
DB 655 GTCTCTTCCAACTCTGTGGACACTCTATTGAGAGGTAGACTATCTTCAAGGAGATCTCTT 714  
QY 721 CCTGGATTAAAGGAACCGCGCATCCCTTTCTATTGAGAAAGTCCACGAGGAAGAGCAGT 780

DB 715 TCTGCATCGACAGAAGTCTCTGCTCTCTTCTTCTTCTAGAGAGCAGAGGAGAGTAGT 774  
QY 781 CTCTCGTGTCTTAAAGACTACATGAGCGGTAGTATCATCCCTTCAAAGTGGGTTC 840  
DB 775 CTCTATGTTTCTCTCAAGAACCAAGATGAATAGCAATACAATTTCTTCCAAAATGGGTTC 834  
QY 841 TTCTGCGCATCAGAAAGCCAGTCTTCCAGAGAGGACGCTGGAGCTTCTCAGAGGC 900  
DB 835 TTCTCCCAATCAGATCTGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
QY 901 AGAAGCTAGCCAGGTCGTAGCTGCTCTCTGAGTCTTTCCTTCTGCTGCTGCTGCTGCT 960  
DB 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTCTGCTGCTGCTGCTGCT 954  
QY 961 TATTGCTGTCTCAAAATGTTCTTCTTCAACTATCGAGAGGAGGAGGAGGAGGAGGAGGAGG 1020  
DB 955 TATTCTCTGTTCAAAATTTGCTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCTTCT 1014  
QY 1021 TGGTACAGCATAGCTTTTGGCTACAGTGGTTCATTTCAATTCATTTCTTCTTCTTCTTCT 1080  
DB 1015 TGGTATAGAAATTCATTTTGGCTTTCAGTGGTTCATTTCTTCTTCTTCTTCTTCTTCTTCT 1074  
QY 1081 CCTTTGTGCCACAGAGGTTTCCAGAAAGGCTTCTTGGAAAGATCTCTGTGTGCAAAAGCAA 1140  
DB 1075 CCATTGTGTACAAAGCGCTTCCAAAGGCTTCTTGAAGATATTTGTATATAAAAGCAA 1134  
QY 1141 CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176  
DB 1135 CCTTACCACATCAACACAGTCGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 1173

RESULT 15  
ADJ26922  
ID ADJ26922 standard; cDNA; 1173 BP.  
XX AC ADJ26922;  
XX AC AC (first entry)  
XX 20-MAY-2004 (first entry)  
DB Human endogenous orphan G-protein coupled receptor RUP7 cDNA.  
XX Human; G protein-coupled receptor; GPCR; dot-blot analysis;  
KW pharmaceutical agent; gene; ss.  
XX Homo sapiens.  
XX Key Location/Qualifiers  
CDS 1..1173  
FT /tag= a  
FT /product= "Human endogenous orphan GPCR protein"  
XX US2003175891-A1.  
XX PN 18-SEP-2003.  
XX PD 21-MAR-2003; 2003US-00393807.  
XX PP 20-NOV-1998; 98US-0109213P.  
XX PR 16-FEB-1999; 99US-0120416P.  
XX PR 26-FEB-1999; 99US-0121852P.  
XX PR 12-MAR-1999; 99US-0123946P.  
XX PR 12-MAR-1999; 99US-0123949P.  
XX PR 28-MAY-1999; 99US-0136436P.  
XX PR 28-MAY-1999; 99US-0136437P.  
XX PR 28-MAY-1999; 99US-0136439P.  
XX PR 28-MAY-1999; 99US-0136567P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137131P.  
XX PR 29-JUN-1999; 99US-0141448P.  
XX PR 28-SEP-1999; 99US-0156333P.  
XX PR 29-SEP-1999; 99US-0156555P.  
XX PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156653P.  
PR 01-OCT-1999; 99US-0157280P.  
PR 01-OCT-1999; 99US-0157281P.  
PR 01-OCT-1999; 99US-0157282P.  
PR 01-OCT-1999; 99US-0157293P.  
PR 01-OCT-1999; 99US-0157294P.  
PR 12-OCT-1999; 99US-00417044.  
PR 17-OCT-2002; 2002US-00272983.  
XX  
PA (CHEN/) CHEN R.  
PA (DANG/) DANG H T.  
PA (LIANW/) LIANW C W.  
PA (LINI/) LIN I.  
XX  
XX Chen R, Dang HT, Liaw CW, Lin I;  
XX  
XX WPI: 2003-898539/82.  
XX P-PSDB; ADJ26923.  
XX  
XX New human G protein-coupled receptor and its coding cDNA, useful for  
XX disease or disorder identification and/or selection, for screening of  
XX candidate compounds useful as pharmaceutical agents, and in research  
XX applications.  
XX  
XX Claim 25; SEQ ID NO 13; 53pp; English.  
XX  
XX The present invention relates to human endogenous orphan G protein-  
XX coupled receptor (GPCR) proteins and polynucleotides encoding such  
XX proteins. The cDNA sequence of the human G protein-coupled receptor  
XX (GPCR) is useful in making a probe for dot-blot analysis against tissue-  
XX mRNA and/or for RT-PCR identification of the expression of the receptor  
XX in tissue samples. GPCR sequences of the invention may be used in  
XX disease/disorder identification and/or selection, in screening of  
XX candidate compounds for use as pharmaceutical agents and in research  
XX settings. The present sequence is human endogenous orphan GPCR cDNA.  
XX  
XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;  
XX  
Query Match 56.9%; Score 669; DB 11; Length 1173;  
Best Local Similarity 74.2%; Pred. No. 3.8e-206;  
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;  
Oy 1 ATGTCGGAGTCTACGGCACTGAGCGTCTTGCCACCTGACTGCTCAAGTCCCTTGGCAATT 60  
Db 1 ATGCCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTGTACTTTAGCAATT 60  
Oy 61 TTAATGCTCCCTGCTTGTCTTGTATACGATGCAATGCTGTGGTCAATTTAGCCCTTT 120  
Db 61 TTTATGCTCTTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCAATTTAGCTTTT 120  
Oy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180  
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Job time : 661 secs

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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

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4: gb\_on.\*  
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6: gb\_pat.\*  
7: gb\_ph.\*  
8: gb\_pl.\*  
9: gb\_pr.\*  
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11: gb\_ats.\*  
12: gb\_sy.\*  
13: gb\_un.\*  
14: gb\_vl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	958.4	81.5	1538	10 AF358859	Mus muscu
3	815.8	69.4	236694	2 AC118386	Rattus no
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6	669	56.9	1173	6 AR142850	Sequence
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8	669	56.9	1173	6 AX109119	Sequence
9	669	56.9	1173	6 AX139113	Sequence
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11	669	56.9	1173	9 AF325356	Homo sapi
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22	669	56.9	1316	9 BC069136	Homo sapi
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ALIGNMENTS

RESULT 1  
AF358860  
LOCUS AF358860 1593 bp mRNA linear ROD 02-SEP-2001  
DEFINITION Rattus norvegicus histamine H4 receptor mRNA, complete cds.  
ACCESSION AF358860  
VERSION AF358860.1 GI:15420536  
KEYWORDS  
SOURCE Rattus norvegicus (Norway rat)  
ORGANISM Rattus norvegicus  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;  
Rattus.

REFERENCE 1 (bases 1 to 1593)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1593)  
AUTHORS Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.  
TITLE Direct Submission  
JOURNAL Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA

FEATURES  
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IATSSRGTHSRRTGLACRSLPGLKEPAAHLSESPRGKSSILVSRTHNSGIIAF  
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RESULT 3

AC118386/c

LOCUS

DEFINITION Rattus norvegicus clone CH230-397N16, \*\*\* SEQUENCING IN PROGRESS

\*\*\*, 3 unordered pieces.

AC118386

VERSION AC118386.4 GI:25013229

KEYWORDS HTG; HTGS PHASE1; HTGS DRAFT; HTGS\_ENRICHED.

SOURCE Rattus norvegicus (Norway rat)

ORGANISM

Rattus norvegicus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;

Rattus.

1 (bases 1 to 236694)

Muzny, D. Marie, Metzger, M. Lee, Abramson, S., Adams, C., Alder, J.,

Allen, C., Allen, H., Alsbrooks, S., Amin, A., Anguiano, D.,

Anyalebechi, V., Aoyagi, A., Ayodeji, M., Baca, E., Baden, H.,

Baldwin, D., Bandaranaike, D., Barber, M., Barnstead, M., Benahmed, F.,

Biswal, K., Blair, J., Blankenburg, K., Blyth, P., Brown, M.,

Bryant, N., Buhay, C., Burch, P., Burrell, K., Calderon, E.,

Cardenas, V., Carter, K., Cavazos, I., Ceasar, H., Center, A.,

Chacko, J., Chavez, D., Chen, G., Chen, R., Chen, Y., Chen, Z., Chu, J.,

Cleveland, C., Cockrell, R., Cox, C., Coyle, M., Cree, A., D'Souza, L.,

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Fraser, C. W., Gabisi, A., Ganta, R., Garcia, A., Garner, T., Garza, M.,

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Liu, J., Liu, Y., Liu, Y., London, P., Longacre, S., Lopez, J.,

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Valas, R., Vera, V., Villaseana, D., Waldron, L., Walker, B., Wang, J.,

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Niederhausern, A., Weiss, R., Smith, D. R., Holt, R. A., Smith, H. O.,

Weinstock, G. and Gibbs, R. A.

Direct Submission

Unpublished

2 (bases 1 to 236694)

Worley, K. C.

Direct Submission

Submitted (17-APR-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA

3 (bases 1 to 236694)

Rat Genome Sequencing Consortium.

Direct Submission

Submitted (15-NOV-2002) Human Genome Sequencing Center, Department

of Molecular and Human Genetics, Baylor College of Medicine, One

Baylor Plaza, Houston, TX 77030, USA



JOURNAL Patent: WO 0185786-A 1 15-NOV-2001;  
American Home Products Corporation (US)  
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RESULT 5  
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DEFINITION Homo sapiens histamine H4 receptor mRNA, complete cds.  
ACCESSION AF307973  
VERSION AF307973.1 GI:11141732  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 1173)  
AUTHORS Jones, P.G., Wu, S. and Betty, M.  
TITLE Cloning of a novel histamine receptor  
JOURNAL Unpublished  
REFERENCE 2 (bases 1 to 1173)  
AUTHORS Jones, P.G., Wu, S. and Betty, M.  
TITLE Direct Submission  
JOURNAL Submitted (25-SEP-2000) Neuroscience, Wyeth Ayerst, CN8000,  
Princeton, NJ 08543, USA  
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Qy 1 ATGTCGAGTCTAAGCGACTGAGCTCTTGCCACTGACTGCTCAAGTCCCTTGGCAATTT 60  
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RESULT 6
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LOCUS
DEFINITION
ACCESSION
AR142850
VERSION
AR142850.1 GI:15104136
KEYWORDS
SOURCE
ORGANISM
Unknown.
Unclassified.
REFERENCE
1 (bases 1 to 1173)
AUTHORS
Behan, J. X., Hedrick, J. A., Laz, T. M., Monema, F. J., Morse, K. L.,
Umland, S. P., and Wang, S.
TITLE
Polynucleotide encoding a histamine receptor
JOURNAL
Patent: US 6204017-A 1 20-MAR-2001;
FEATURES
Location/Qualifiers
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Query Match 56.9%; Score 669; DB 6; Length 1173;
Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
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DB 477 --TGAAGGTAGTGAATGTGAACCTGGATTTTTTTCGGAATGGTACATCCTTGCATCACA 534
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QY	781	CTCCTGGTGTCTTAAAGGACTCACAATGAGCGGTAGTATCATCGCTTTCAAAGTGGGTTC	840
DB	775	CTCATGTGTTTCTTCAGAAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC	834
QY	841	TTCTGCCGATCAGAAAGCCAGTCTTCCACAGAGAGACACGTGGAGCTTCTCAGAGGC	900
DB	835	TTCTCCCAATCAGATCTCTGAGTCTTTCACAAAGGGAACATGTTGAATGCTTAGAGCC	894
QY	901	AGGAAGTACGCCAGGTCGTAGTGTCTCTCGAGTCTTTTGCCATTTGCTGGGCTCCG	960
DB	895	AGGAGATTACCCAAGTCACTGGCCATTTCTCTTAGGGGTTTTTGCTGTTTCTGGGCTCCA	954
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QY	1021	TGTTACAGCATAGCTTTTGGCTACAGTGGTTCAAATTCACTTAATCCCTTTCTATAC	1080
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DEFINITION	Sequence 1 from patent US 6613533.		linear
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ACCESSION      AR391860
VERSION        AR391860.1  GI:40115588
KEYWORDS
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REFERENCE      1 (bases 1 to 1173)
AUTHORS        Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
                Umland,S.P. and Wang,S.
TITLE          Histamine receptor
JOURNAL        Patent: US 6613533-A 1 02-SEP-2003;
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Db	121	GTGTGGGACAAAAA	CCTTAGACAT	CGAAGTAG	TTATTTTTT	CTCTTAATTTTGG	CGCAATCTCT	180	
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Db	241	GAATTTGGAAAGGAAATCTGTGATTTTGGCTCACTACTGACTATCTGTATTGTACAGCA	300
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Db	301	TCTGTATATAACATTTGTCCTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG	360
Qy	361	CGTTATAGACACAGCACACTGGCATCTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG	420
Db	361	TCATTATAGAACTCAACATACTGGGCTCTGGAATTTGTTACTCTGATGGTGGCCGTTTGG	420
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Qy	961	TATTGCTGTTCACAAATGTTCTTTTCAATATCGCAGAGGGGAGCGCCCAAAATCGATT	1020
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ACCESSION	AX109119		
VERSION	AX109119.1	GI:13924093	
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SOURCE         Homo sapiens
ORGANISM       Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
               Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE     1
AUTHORS       Behan, J.X., Hedrick, J.A., Laz, T.M., Monsma, F.J., Morse, K.L.,
               Umland, S. and Wang, S.
TITLE         Histamine receptor
JOURNAL       Patent: WO 0125432-A 1 12-APR-2001;
               SCHERING CORPORATION (US)
FEATURES      Location/Qualifiers
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Query Match      56.9%; Score 669; DB 6; Length 1173;
Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

QY 1 ATGTCGGAGTCTAACGGCACTGACGCTTCCCACTGCTCTCAAGTCCCTTGGCAATTT 60
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QY 901 AGAAGCTAGCCAGGTGCGTAGCTGCTCTCGTAGTGTCTTTGGCCATTTGCTGGGCTCCG 960
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1075 CCATTGTGTCAAAAGCGCTTCAAAGAGGCTTCTTGAAGATATTTGTATAAAAAGCAA 1134
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 1141 CCAGCACCTTC---ACAGACCCAGTCAGTATCTTCTTGA 1176
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||

RESULT 9
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LOCUS      AX139113                1173 bp      DNA      linear      PAT 30-MAY-2001
DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION  AX139113
VERSION     AX139113.1 GI:14274791
KEYWORDS
SOURCE      Homo sapiens (human)
ORGANISM    Homo sapiens
            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
            Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE   1
AUTHORS     Peter, B. and O'Reilly, M.A.
TITLE       G-protein coupled receptor-like polypeptide
JOURNAL     Patent: EP 1096009-A 1 02-MAY-2001;
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Query Match      56.9%; Score 669; DB 6; Length 1173;
Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;

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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTTCT 180
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTATTTTCTTAACTTGGCCATCTCT 180
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 181 GACTTCTTGTGGTGTGCTCTCCATTCCTCTGTATACCTCCACACGCTGTTTAACCTGG 240
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 AATTTTGGAGTGGAACTCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTCCACAGCA 300
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 TCGTCTACAGTATGTCTCTCATTAGCTACGATCGATACGACGTCAGTTCAAAACGCTGTG 360
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
QY 301 TCTGTATATAACATGTCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360
DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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DB ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
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Db	361	TCTTATAGAACTCAACATACTGGGCTCTTGAAGATTGTTACTCTGATGGTGGCGTTGG	420
QY	421	ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATCTTGGNAGAACAGC	480
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QY	481	ACCAACACAGAGGAGTGGAGCTGGCTTTGTTACTGAGTGATGATACCTCGCCATTACA	540
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QY	541	GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTTCAGTGTACAGATTTAC	600
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QY	601	TGGAGCTGTGGAAGCGTGGAGTCTCAGTAGGTGCCCTAGCCAGCTGGATTCATCGCT	660
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QY	1021	TGGTACAGTACGCTTTTGGCTACAGTGGTTCAATTCATTTAATCCCTTCTATAC	1080
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RESULT 10			
BD015847			
LOCUS			
DEFINITION			
ACCESSION			
VERSION			
KEYWORDS			
SOURCE			

ORGANISM	Homo sapiens									
REFERENCE	Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.									
AUTHORS	1 (bases 1 to 1173)									
TITLE	Peter, B. and Olaylee, M.A.									
JOURNAL	Novel polypeptide									
COMMENT	Patent: JP 2001211889-A 1 07-AUG-2001; PFIZER INC									
OS	Homo sapiens (human)									
PN	JP 2001211889-A/1									
PD	07-AUG-2001									
PF	27-OCT-2000 JP 2000329359									
PR	29-OCT-1999 GB 9925641.4, 20-APR-2000 GB 0009973:9 PI									
PC	BEAT PETER, MARK ANTONY OLAYLEE									
PC	C12N15/09, A61K38/00, A61K39/395, A61K48/00, A61P1/04, A61P11/00,									
PC	A61P11/06, A61P29/00, A61P31/00, A61P35/00, A61P37/02, A61P37/08, C07K14/00,									
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Query Match	56.9%; Score 669; DB 6; Length 1173;									
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Matches	875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;									
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QY	241	AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCA	300							
Db	241	GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA	300							
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RESULT 11
AF325356 1173 bp mRNA linear PRI 11-SEP-2001
LOCUS Homo sapiens histamine receptor H4 (AXOR35) mRNA, complete cds.
DEFINITION AF325356
ACCESSION AF325356
VERSION AF325356.1 GI:15553202
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 1173)
Zhu, Y., Michalovich, D., Wu, H.-L., Tan, K.B., Dytko, G.M.,
Mannan, I.J., Boyce, R., Alston, J., Tierney, L.A., Li, X.,
Herrity, N.C., Vawter, L., Sarau, H.M., Ames, R.S., Davenport, C.M.,
Hieble, P., Wilson, S., Bergsma, D.J. and Fitzgerald, L.R.
Cloning, expression, and pharmacological characterization of a
novel human histamine receptor
Mol. Pharmacol. 59 (3), 434-441 (2001)
21106320
PUBMED 11179436
2 (bases 1 to 1173)
Zhu, Y., Michalovich, D. and Fitzgerald, L.R.
Direct Submission
TITLE Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box
1539, King of Prussia, PA 19406, USA
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ORIGIN
Query Match 56.9%; Score 669; DB 9; Length 1173;
Best Local Similarity 74.2%; Pred. No. 9.4e-191;
Matches 875; Conservative 0; Mismatches 295; Indels 9; Gaps 2;
Qy 1 ATGTGCGAGTCTTAACCGCACTGACGCTTCCGCACTGACTGCTCAAGTCCCTCTGGCAATTT 60
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RESULT 12
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LOCUS Homo sapiens histamine receptor H4 mRNA, complete cds.
DEFINITION AF329449
ACCESSION AF329449
VERSION AF329449.1 GI:13876643
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Morse,K.L., Behan,J., Laz,T.M., West,R.E. Jr., Greenfeder,S.A.,
Anthes,J.C., Umland,S., Wan,Y., Hipkin,R.W., Gonsiorek,W., Shin,N.,
Gustafson,E.L., Qiao,X., Wang,S., Hedrick,J.A., Greene,J., Bayne,M.
and Monsma,F.J. Jr.
Cloning and characterization of a novel human histamine receptor
J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)
21104636
MEDLINE
PUBMED 11181941
REFERENCE 2 (bases 1 to 1173)
AUTHORS Monsma,F.J. Jr., Wang,S., Behan,J., Laz,T.M., Greene,J. and
Bayne,M.
TITLE Direct Submission
JOURNAL Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough
Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033,
USA
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 VERSION AY008280.1 GI:15822540  
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 SOURCE  
 ORGANISM Homo sapiens (human)

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
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 1 (bases 1 to 1173)  
 Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K.,  
 Cheng,R., Rauser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and  
 O'Dowd,B.P.

TITLE Discovery of a novel member of the histamine receptor family  
 JOURNAL Mol. Pharmacol. 59 (3), 427-433 (2001)  
 MEDLINE 21106319  
 PUBMED 11179435

2 (bases 1 to 1173)  
 Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and  
 O'Dowd,B.P.  
 AUTHORS  
 Discovery of H4, a Novel Histamine Receptor

TITLE Unpublished  
 JOURNAL  
 3 (bases 1 to 1173)  
 Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and  
 O'Dowd,B.P.

TITLE Direct Submission  
 JOURNAL Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8  
 Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada  
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## gene

## CDS

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ACCESSION	AJ298292
VERSION	AJ298292.1 GI:18152452

KEYWORDS	histamine receptor H4; HRH4 gene.
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REFERENCE	1 O'Reilly, M.A. Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis Unpublished
JOURNAL	2 (bases 1 to 1173)
REFERENCE	O'Reilly, M.A. Direct Submission Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer Ltd, Ramesgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM
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GenCore version 5.1.6  
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OM nucleic - nucleic search, using sw model

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Listing first 45 summaries

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5: gb\_est4.\*  
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7: gb\_est6.\*  
8: gb\_ges1.\*  
9: gb\_ges2.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

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#### ALIGNMENTS

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VERSION BX643713  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1 (bases 1 to 839)  
AUTHORS Fobo G., Han, M. and Wiemann, S.  
TITLE EST (Lauber, J., Bahr, A., Mewes, H.W., Weil, B., Amid, C., et al.)  
JOURNAL Unpublished (2003)  
COMMENT Contact: MIPS  
MIPS Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany  
This is the 5' sequence of the clone insert  
Clone from S. Wiemann, Molecular Genome Analysis, German Cancer  
Research Center (DKFZ); Email s.wiemann@dkfz-heidelberg.de;  
sequenced by Qiagen (Hilden/Germany) within the cDNA sequencing  
consortium of the German Genome Project.  
No sl sequence available.  
This clone (DKFZp781C0629) is available at the RZPD in Berlin.  
Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059  
Berlin-Charlottenburg, GERMANY; Email: clone@rzpd.de.

FEATURES  
source  
1..839  
/organism="Homo sapiens"  
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/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="781 (synonym: hlcc4)"  
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cDNA-collection"

#### ORIGIN

Query Match 37.2%; Score 437; DB 5; Length 839;  
Best Local Similarity 75.8%; Pred. No. 9.8e-120;  
Matches 569; Conservative 0; Mismatches 175; Indels 7; Gaps 2;

Qy 1 ATGTCGGAGTCTAACGGCACTGACGCTTGCCACTGACTGCTCAAGTCCCTTGGCATTT 60

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Db 96 ATCCGATACATAAGCAATCAATTAATCACTAGCACTCTGTACTTTAGCATTT 155
Qy 61 TTAATGTCCTGCTGTTGCTTTGCTATACGATAGCAATGCTGTGTCATTTAGCCTTT 120
Db 156 TTTATGTCCTTAGTAGCTTTTGTCTAATGCTAGCAATGCTTGGTCATTTAGCTTTT 215
Qy 121 GTAGCAGACAGAACCTTAGACATCGAAGTAATTTATTTTCTTAATTTGGCTATTCT 180
Db 216 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAATTTGGCCATCTCT 275
Qy 181 GACTTCTTCGTGGGTGATCTCTCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 240
Db 276 GACTTCTTCGTGGGTGATCTCTCATTCCTCTGTACATCCCTCACAGCTGTTTAACTGG 335
Qy 241 AATTTGGAAGTGGAATCTGCAATGCTTTTGGCTCAATTAAGTATCTTTTGTGCACAGCA 300
Db 336 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 395
Qy 301 TCCGCTACAGATTGTCCTCATCTAGCTAGCATCGATACAGTACAGTTCAGACGCTGTG 360
Db 396 TCTGTATATACATGTCCTCATCTAGCTAGCATCGATACAGTTCAGTTCAGTTCAGTTC 455
Qy 361 CGTTATAGACACAGCACACTGGCATCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGG 420
Db 456 TCTTATAGAACTCAACATCTGGGCTCTTGAAGATTCTTACTCTGATGTTGGCGTGG 515
Qy 421 ATACTGCTTCTTGGTCAATGCGCCAAATGATTCGCTGCGGATTCGGAATCTTGAAGAAC 480
Db 516 GTGTGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTCAGAGTCTTGAAGAGTAA 575
Qy 481 ACCAACACAGAGGAGTGGGAGCTGCTTCTTACTAGTGGTACATCCCTCGCATTAACA 540
Db 576 GTTA-----GTGAATGTGAACCTGGATTTTTCGGAATGGTACATCCCTTGGCCATCACA 629
Qy 541 GCATTTCTTGAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTCAAGTGACAGATTAC 600
Db 630 TCATTTCTTGAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTCAAGTGACAGATTAT 689
Qy 601 TGGAGCTCTGGAAGCTGGAGTCTCAGTAGTGGCTTACGCTAGCCAGCTGATTCATCGCT 660
Db 690 TGGAGCTCTGGAAGCTGGAGTCTCAGTAGTGGCTTACGCTAGCCAGCTTCTGGAAGCT 749
Qy 661 ACCTTCTCCAGGAGCTAGACACTCAGCAGACTCGGTTGGCTTGTAGACAGTCTT 720
Db 750 GTCTCTTCCA-CATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGAGATCTCTT 808
Qy 721 CCTGGATTAAAGGAACCGACCGCATCCCTTC 751
Db 809 TCTGCATCGACAGAAATTCCTGCATCCTTTC 839

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RESULT 2
CF147821 704 bp mRNA linear EST 25-JUL-2003
LOCUS AGENCOURT 1470195 NIH MGC 145 Homo sapiens cDNA clone
DEFINITION IMAGE.6971900 5', mRNA sequence.
ACCESSION CF147821
VERSION CF147821.1 GI:33244089
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 704)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cga@nci.nih.gov

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FEATURES
    source            1..704
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    mol_type="mRNA"
    db_xref="taxon:9606"
    clone="IMAGE:6971900"
    tissue_type="mixed"
    lab_host="DH10B"
    clone_lib="NIH MGC 145"
    notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:
    varies by clone; ORFs were PCR-amplified and cloned into
    pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
    clone and include the following: 5'-EcoRV-Xmi/NotI-3',
    5'-EcoRV-Xmi/NotI-3', EcoRV (TA cloned, non-directional).
    For information about which gene each clones represents,
    please visit our anonymous ftp site at
    ftp://image.llnl.gov/image/rearrayed_plates/IRAI.preSV.dat
    a Note: this is a NIH_MGC Library."
    Query Match      35.7%; Score 420; DB 7; Length 704;
    Best Local Similarity 76.5%; Pred. No. 1.2e-114;
    Matches 543; Conservative 0; Mismatches 160; Indels 7; Gaps 2;

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ORIGIN
Qy 3  GTCGAGTCTAACGGCACTGACGCTCTTGGCCACTGCTCAAGTCTCAAGTCCCTTGGCATTTT 62
Db 1  GCCAGATACCTAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTTT 60
Qy 63  AATGTCCTCTGCTTCTTCTTATACGATAGCAATGCTGTGCTATTTTGGCTTTT 122
Db 61  TATGTCCTTAGTAGTCTTCTTCTTATATGCTAGGAATGCTTTGCTCAATTTTGGCTTTT 120
Qy 123 AGCAGACAGAAAACCTTAGACATCGAAGTAATTTTCTTAAATTTGGCTATTTCTGA 182
Db 121 GGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACTTGGCCATCTCTGA 180
Qy 183 CTTCTTCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTCGAA 242
Db 181 CTTCTTCTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTCGAA 240
Qy 243 TTTTGGAAAGTGGAACTGCAATGTTTGGCTCATTTACTGACTATCTTTTGTGACAGCATC 302
Db 241 TTTTGGAAAGAAATCTGTATTTTGGCTCATTTACTGACTATCTTTTGTGACAGCATC 300
Qy 303 CGTCTACAGTATTTCTCTCATTTAGTACGATACGATACAGTCTAGTCTTCAACGCTGTGCG 362
Db 301 TGTATATAACATTTGCTCTCATCAGCTATGATGATACATCTGCTAGTCTCAAAATGCTGTG 360
Qy 363 TTATAGACACAGCACTCTGGCATCTGGAATTTTGTGCTCAAAATGCTGTGCTGTTTGGAT 422
Db 361 TTATAGAACTCAACATCTGGGTCTTGAAGATTTGTTACTCTGATGCTGGCGTGGGT 420
Qy 423 ACTGGCTTCTTGGTCAATGCGCCAAATGTTCTGGCTTCGATTTCTTGGAAAGACAGCAC 482
Db 421 GCTGGCTTCTTGTAGTAATGGGCAATGATTTCTAGTTTCAGAGTCTTGGAAAGG----- 474
Qy 483 CAACACAGAGAGTGGCAGCTCTGGCTTTTGTACTGAGTGGTGTACATCTCGCCATTACAGC 542
Db 475 TGAAGGTAGTGAATGTGAACCTGGAATTTTTCGGAATGTTTACATCTTGCATCATCATC 534
Qy 543 ATTCTTGGAAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 602
Db 535 ATTCTTGGAAATTCCTGCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 594

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Tissue Procurement: GPCR Consortium
cDNA Library Preparation: GPCR Consortium
DNA Sequencing by: The I.M.A.G.E. Consortium (LLNL)
Cloning by: Agencourt Bioscience Corporation
Cloning through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB102 row: b column: 07
High quality sequence stop: 685.
Location/Qualifiers
    1..704

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Qy 603 GAGCTGTGGAAGCGTGGAGTCTCAGTAGTGCCCTAGCCACGCTGGATTCAATCGCTAC 662
Db 595 GAGCGTGTGGAAGCGTGTATCATCTCAGTAGTGCCCAAGCCATCCTGACTGACTGCTGT 654
Qy 663 CTCCTCCAGGGGCACTGACACTCAGCAGAACTGGGTTGGCTTGTAGGA 712
Db 655 CTCCTCCA-CATCTGTGGACACTATTCAGAGGTAGACTATCTTTCAGGA 703

RESULT 3
LOCUS CO959034
DEFINITION AGNCOURT_30842625 NIH_MGC_146 Homo sapiens cDNA clone
IMAGE:7389774 5', mRNA sequence.
ACCESSION CO959034
VERSION CO959034.1 GI:51323616
KEYWORDS EST.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE 1 (bases 1 to 721)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Guthrie cDNA Resource Center
cDNA Library Preparation: Guthrie cDNA Resource Center
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: IRB18 row: a column: 04
High quality sequence start: 2
High quality sequence stop: 328.
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/clone="IMAGE:7389774"
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/clone_lib="NIH_MGC_146"
/note="Vector: pCDNA3.1; Site_1: multiple; Site_2:
multiple; ORF's were PCR-amplified (from IMAGE clones or
from commercially available cDNA libraries) and cloned by
the Guthrie cDNA Resource Center (www.guthrie.org/cDNA)
into pCDNA3.1. For specific information on cloning sites
(which vary by clone), please refer to the Guthrie
website, using the Guthrie ID given in the file
ftp://image.llnl.gov/image.rearrayed_plates/IRBP.presv.dat
a. Note: this is a NIH_MGC Library."

ORIGIN
Query Match 21.5%; Score 253.2; DB 7; Length 721;
Best Local Similarity 77.7%; Pred. No. 2.2e-64;
Matches 306; Conservative 0; Mismatches '88; Indels 0; Gaps 0;

Qy 1 ATGTCGGAGTCAAGCGCACTGAGCTCTTGGCACTGCTCAAGTCCCTGGCAATTT 60
Db 22 ATGCCAGATACATAAGCACAAATCAATTTATCAAGCACTCGGTACTTTAGCAATTT 81
Qy 61 TTAATGTCCTCGCTTGTCTTGTCTATAACGATAGGCAATGCTGTGTCATTTTAGCCCTTT 120
Db 82 TTTATGTCCTTAGTAGCTTTTGTCTATATGCTAGGAATGCTTTGGTCATTTTAGCTTTT 141
Qy 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAAATTTATTTTCTTTAAATTTGGCTATTTCT 180

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Db 142 GTGGTGACAAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCCATCTCT 201
Qy 181 GACTTCTTGGTGGGTGTCATCTCCATTCTCTGTACATCCCTCACACGCTGTTTAACTGG 240
Db 202 GACTTCTTGGTGGGTGTCATCTCCATTCTCTGTACATCCCTCACACGCTGTTTAACTGG 261
Qy 241 AATTTTGGAAAGTGAATCTGCATGTTTTGGTGCATCTACTGACTATCTTTTGTGCACAGA 300
Db 262 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACCGCA 321
Qy 301 TCCGCTCTACAGTATTGCTCCTCATTTAGCTACCATCGATACCATGAGTTTCAACGCTGTG 360
Db 322 GCTGTATATAGATTGCTCCTCATCAGCTATCATAAATACCTGTCAATCTCAATGCTTTG 381
Qy 361 CGTTATAGAGCACAGCACACTGGCATCTCTGAAAA 394
Db 382 TCTTATGGAACGCAAAAAACGGGGGCTGAAGA 415

RESULT 4
LOCUS CD326085
DEFINITION AGNCOURT_14163426 NIHCD_XGC_Eyel Xenopus laevis cDNA clone
IMAGE:6949081 5', mRNA sequence.
ACCESSION CD326085
VERSION CD326085.1 GI:31090416
KEYWORDS EST.
SOURCE Xenopus laevis (African clawed frog)
ORGANISM Xenopus laevis
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Amphibia; Batrachia; Anura; Mesobatrachia; Pipoidae; Pipidae;
Xenopodinae; Xenopus; Xenopus.
REFERENCE 1 (bases 1 to 853)
AUTHORS NIH-MGC http://mgi.nci.nih.gov/.
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)
JOURNAL Unpublished (1999)
COMMENT Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement:
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM14564 row: f column: 24
High quality sequence stop: 707.
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Location/Qualifiers
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/clone="IMAGE:6949081"
/dev_stage="adult"
/lab_host="DH10B (phage-resistant)"
/clone_lib="NIHCD_XGC_Eyel"
/note="Organ: eye; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: SalI; Cloned unidirectionally. Primer: Oligo dn.
Average insert size 2.3 kb. Constructed by Life
Technologies. Note: This is a Xenopus Gene Collection
(XGC) library."

ORIGIN
Query Match 11.3%; Score 133; DB 6; Length 853;
Best Local Similarity 59.3%; Pred. No. 3.7e-28;
Matches 245; Conservative 0; Mismatches 165; Indels 3; Gaps 1;

Qy 46 GTCCCTTGGCAATTTTAAATGCTCCTGCTTTGTCTATACGATAGGCAATGCTGTG 105

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Db      382 GTCTTCCTGCTGCTCCTCATAGTTAGACCGCTGCTGGGAATGCCCTG 441
Qy      106 GTCAATTTAGCCTTTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTT 165
Db      442 GTCATGCTGCTTTTGTGTGAGCTCCAGCCTCCGAAACCCAGAAATATTTCTCTC 501
Qy      166 AATTTGGCTATTTCTGACTTTCTGCTGGTGTCACTCTCCATCTCTGTACATCCCTCAC 225
Db      502 AACTGGCTATCTCAGATTTCTTTGTAGTGCCCTGTGCACTCCCTCTGTATGTGCCATAC 561
Qy      226 ACGCTGTTT---AATCGAAATTTTGGAAAGTGGAACTCTGCAATGTTTGGCTCAATCTACTGAC 282
Db      562 GTACTGACTGGCAGATGGAGCTTTGGCAGGAGCGTTTGGAAACTGTGGCTGTTCTGGAT 621
Qy      283 TATCTTTTGTGCACAGATCGGTCTACAGTATGTCTCTCAATAGCTAGGATCGATACACAG 342
Db      622 TATCTGCTCTGCACCTCGTCCGTGTTCAACATCGTGTCTCATCAGCTACGACAGGTTTCATC 681
Qy      343 TCAGTTTCAAAACGCTGTGCGTTATAGACACAGCACACTGGCATCTCGTAAATTTGTTGCT 402
Db      682 TCTGTGACCCGGCTGTCAAGTACCGAGCTCAGCAGAGTAACAGCCGGCATGCACTTTG 741
Qy      403 CAAATGCTGCTGTTTGGACTACTGGCTTCTTGGTCAATGGCCCAATGATTCT 455
Db      742 AAAATGACCATGCTGTGATCTTGGCTTCTCTCTATATGACCCAGCCATTAT 794

RESULT 5
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LOCUS
DEFINITION
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  CB556920
ACCESSION
  CB556920
VERSION
  CB556920.1 GI:29496320
KEYWORDS
  EST.
SOURCE
  Rattus norvegicus (Norway rat)
ORGANISM
  Rattus norvegicus
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
  Rattus.
REFERENCE
  1 (bases 1 to 672)
  Angen EST Program.
  Angen Rat EST Program
  Unpublished (2003)
  Contact: Dan Fitzpatrick
  Angen, Inc
  One Angen Center Drive, Thousand Oaks, CA 91320-1799, USA
  Tel: 805 447-4881
  Plate: 00001 row: d column: 6.
  Location/Qualifiers
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FEATURES
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ORIGIN
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  Best Local Similarity 58.7%; Pred. No. 1.4e-27;
  Matches 246; Conservative 0; Mismatches 170; Indels 3; Gaps 1;

Qy      51 CTTGGCAATTTTAAATGCTGCTGCTTTTGTGCTATAACGATAGCAATGCTGGTGCAT 110
Db      226 CTTGGCTGCGCTCATGGCGCTGCTCATGCTGGCCACAGTACTGGCAACGGCTGGTGCAT 285
Qy      111 TTTAGCTTTGTAGACACAGAAACCTTAGACATCGAGTAATATTTTCTTAATTT 170
Db      286 GCTCGCTTTGTGGCGAATTCGACCTCCGACCCAGAACAACTTCTTCTGCTCAACCT 345
Qy      171 GGCTATTTCTGACTTCTTCTGCTGGGTGTCATCTCCATTCTCTGTATACCTCCCTCACAGCT 230

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Db      346 CGCATCTCGACTTCTCTGTGGTGCCCTTCTGCATCCCATTTGTAGTACCTATGTGCT 405
Qy      231 GTTTAAAC---TGGAAATTTTGGAAAGTGGAAATCTGCATGTTTGGCTCATTAAGTACTATCT 287
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Qy      288 TTTGTGCACAGCATCGTCTACAGTATTTGCTCTCATTAAGCTAGCTAGCATGATACCAAGTCAGT 347
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Qy      348 TTCAAACGCTGTGCTTTATAGACACAGACACTGGCATCTCTGAAATTTGTTGCTCAAT 407
Db      526 CATCTGAGCTGTCTCTTACAGGCCAGAGGGGGACACAGAGCGGCCCTTCGGAGAT 585
Qy      408 GGTGGCTGTTTGGATCTAGCTTTTCTGTTGTTCAATGGCCCAATGATTCTGGCTTGGGATT 466
Db      586 GGCACCTGGTGTGGTGTCTGCTTCTGCTGTATGGCTTGCCTCATCTGAGTTGGGAGT 644

RESULT 6
CF147822
LOCUS
DEFINITION
  AGENCOURT 14740187 NIH MGC 145 Homo sapiens cDNA clone
  CF147822
ACCESSION
  CF147822
VERSION
  CF147822.1 GI:3244090
KEYWORDS
  EST.
SOURCE
  Homo sapiens (human)
ORGANISM
  Homo sapiens
  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
  Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
REFERENCE
  1 (bases 1 to 732)
  NIH-MGC http://mgi.nci.nih.gov/.
  National Institutes of Health, Mammalian Gene Collection (MGC)
  Unpublished (1999)
  Contact: Daniela S. Gerhard, Ph.D.
  Office of Cancer Genomics / NIH
  National Cancer Institute / NIH
  Bldg. 31 Rm10A07 Bethesda, MD 20892
  Email: cgapbs-x@mail.nih.gov
  Tissue Procurement: GPCR Consortium
  cDNA Library Preparation: GPCR Consortium
  CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
  DNA Sequencing by: Agencourt Bioscience Corporation
  Clone distribution: MGC clone distribution information can be
  found through the I.M.A.G.E. Consortium/LLNL at:
  http://image.llnl.gov
  Plate: IRBI02 row: b column: 06
  High quality sequence stop: 610.
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      /mol_type="mRNA"
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      /clone="IMAGE:6971899"
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      /note="vector: pCDNA3.1; Site 1: varies by clone; Site 2:
      varies by clone; ORFs were PCR-amplified and cloned into
      pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
      clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
      5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
      For information about which gene each clones represents,
      please visit our anonymous ftp site at
      ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat
      a Note: this is a NIH_MGC Library."

FEATURES
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      varies by clone; ORFs were PCR-amplified and cloned into
      pCDNA3.1 by the GPCR Consortium. Cloning sites vary by
      clone and include the following: 5'-EcoRV-XmnI/XhoI-3',
      5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).
      For information about which gene each clones represents,
      please visit our anonymous ftp site at
      ftp://image.llnl.gov/image/rearrayed_plates/IRBI.presv.dat
      a Note: this is a NIH_MGC Library."

ORIGIN
  Query Match 11.0%; Score 129.4; DB 7; Length 732;
  Best Local Similarity 57.0%; Pred. No. 4.3e-27;
  Matches 257; Conservative 0; Mismatches 191; Indels 3; Gaps 1;

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QY 53 TGGCATTTTAAATGCTCCTGCTGTTTGTCTATACGATAGGCAATGCTGTGTCATTT 112
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Db 126 TGGCGCGCTCATGGCGTGTCTATCGTGGCCAGCGTGTGGCAAGCGCTGTCATGC 185
|||
QY 113 TAGCCTTTAGCAGACAGAACTTACATCGAAGTAATATTTTCTTAATTTGG 172
|||
Db 186 TCGCCTTCGTGGCGAGCTGAGAGCTCGCAGCCACCAACAACCTTCTTCTGCTCAACCTCG 245
|||
QY 173 CTATTTCTGACTTCTTCTGCTGGGTGTCATCTCCATCTCTGTATACATCCCTCACAGCTG- 231
|||
Db 246 CCATCTCCGACTTCTCTGCTGGCGCTTCTGCATCCCACTGTATGACCTACGCTGTA 305
|||
QY 232 --TTTAACTGGAATTTGGAAAGTGAATCTGCATGTTTGTGCTCATCTACTATCTTT 289
|||
Db 306 CAGGCCGTGGACCTTCGGCGGGGCTCTGCAAGCTGTGGCTGTGTAGTGACTACCTGC 365
|||
QY 290 TGTGCACAGCATCGTCTACAGTATGTCCTCATCTAGTACGATCGATACAGTCAGTTT 349
|||
Db 366 TGTGCACCTCTCTGCTTCAACATCGTGTCTATCAGCTAGCAGCGCTTCTGCTGGTCA 425
|||
QY 350 CAACAGCTGTGCGTTATAGACACAGCACACACTGGCATCTCTCAAAATTTGTTGCTCAAATGG 409
|||
Db 426 CCGAGCGTCTCATACCGGCCACAGAGGTGACACGGCGGCGAGTGGCGAATGC 485
|||
QY 410 TGGCTGTTGATCTGCTTCTTGTGTCATGTCATGTCCTCAATGCCCAATGATCTGCTTCGATCTTT 469
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Db 486 TGTGCTGTGGTGTGCTGCTGCTTCTGCTGTACGACAGCAGCATCTGAGCTGGAGTACC 545
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QY 470 GGAGACACAGCAACACACAGAGAGTCCGA 500
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Db 546 TGTCCGGGGCAGCTCCATCCCGAGGGCCA 576
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RESULT 7
CC481311 584 bp DNA linear GSS 16-JUN-2003
LOCUS CH240_309C10.T7 CHORI-240 Bos taurus genomic clone CH240_309C10,
genomic survey sequence.
CC481311
CC481311.1 GI:31760574
GSS.
SOURCE Bos taurus (cow)
ORGANISM Bos taurus
REFERENCE
AUTHORS Holt,R., Stott,J., Yang,G., Barber,S., Smailus,D., Prabhu,A.-L.,
Teai,M., Cloutier,A., Lee,D., Girn,N., Olson,T., Mayo,M.,
Butterfield,Y., Kirkpatrick,R., Liu,J., Guin,R., Chan,A., Chiu,R.,
Mathewson,C., Wye,N., Masson,A., Brown-John,M., Jones,S.,
Schein,J., Warra,M., de Jong,P., McWilliam,S., Barris,W.,
Dalrymple,B.P. and Tellam,R.
1 (bases 1 to 584)
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Cetartiodactyla; Ruminantia; Pecora; Bovidae;
Bovinae; Bos.
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..643
/organism="Xenopus tropicalis"

TITLE
JOURNAL
COMMENT
Other GSSs: CH240_309C10.TARBAC13P2
Contact: Rob Holt
Sequencing
The British Columbia Cancer Agency Genome Science Centre
600 W. 10th Ave, Vancouver, British Columbia, Canada V5Z 4E6
Tel: 604-877-6085
Fax: 604-877-6276
Email: rholt@bcgsc.ca
Clones are derived from the bovine BAC library CHORI-240
(http://www.chori.org/bacpac/bovine240.htm). For BAC library
availability, please contact Pieter de Jong (pdejong@gmail.com).
Clones may be purchased from BACPAC Resources
(http://www.chori.org/bacpac/ordering/information.htm). This work
was undertaken as part of the International Bovine BAC Mapping
Consortium (IBBMC) by CSIRO Livestock Industries, Australia and the
British Columbia Genome Sciences Centre, Canada.
Plate: 309 row: C column: 10
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Seq primer: T7
Class: BAC ends.
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/mol_type="genomic DNA"
/strain="breed: Hereford"
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/clone="CH240_309C10"
/sex="Male"
/cell_type="Blood"
/clone_lib="CHORI-240"
/notes="vector: pTARBAC1.3; Site 1: MboI; Site 2: MboI;
Hereford bull L1 Domino 99375; CHORI-240 Bovine BAC
library (Male) produced by Pieter de Jong"

ORIGIN
Query Match 9.8%; Score 115.6; DB 9; Length 684;
Best Local Similarity 70.6%; Pred. No. 6e-23;
Matches 154; Conservative 0; Mismatches 64; Indels 0; Gaps 0;

QY 150 TAATATATTTTCTTAATTTGGCTATTTCTGACTTCTTCTGTTGGTGTCTATCTCCATTC 209
|||
Db 260 TACGTGCTATATTGTTAACTTCTTCTTTCGCCCATGCAGGTATGATCTCCATTC 319
|||
QY 210 TCTGTACATCCCTCACAGCTGTTTAACTGGAATTTTGGAAAGTGGAAATCTGCATGTTT 269
|||
Db 320 TTTATTATCCCTCACAGCTCTTCAACTGGAGTTTGAATAAATAACATTTGTGCTTTTG 379
|||
QY 270 GCTCATTTACTGACTATCTTTTGTGCACAGCATCGTCTACAGTATTGCTCTCATAGCTA 329
|||
Db 380 GCTCAGTACTGACTATCTTTTGTGTACAGCATCTGTGTATAACATCGTACTCATCAGCTT 439
|||
QY 330 CGATCGATACAGTCAGTTTCAAAACGCTGTGCGTTATA 367
|||
Db 440 TGATCGATATCAGTCAGTCTCCAATGCTGTAAAGTCAA 477
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RESULT 8
AL848045 643 bp mRNA linear EST 26-NOV-2003
LOCUS AL848045 XGC-egg Xenopus tropicalis cDNA clone TEGG022122 5', mRNA
sequence.
AL848045
AL848045.2 GI:38559584
ACCESSION
VERSION
KEYWORDS EST.
SOURCE
ORGANISM Xenopus tropicalis (western clawed frog)
REFERENCE
AUTHORS Croning,M.D.R., Ashurst,J.L., Taylor,R., Zorn,A.M. and Rogers,J.
1 (bases 1 to 643)
Sanger Xenopus tropicalis EST project 2001 (11_2003)
Unpublished (2003)
On Sep 15, 2002 this sequence version replaced gi:22868110.
Contact: Taylor R
Sanger Institute
Hinxtion, Cambridgeshire, CB10 1SA, UK
Email: tropesanger.ac.uk
Sanger Xenopus tropicalis EST project 2001
TROPICALIS_SEQUENCE ID: TEGG022122.plkSP6
Sequencing primer: SP6
This sequence is from a Xenopus Gene Collection (XGC) library
constructed by Aaron M. Zorn.
cDNA was oligo dT primed from 5ug of poly A+ RNA from egg.
ECORI-NotI cut cDNA was then ligated into pCS107 with EcoRI at the
5' end and NotI at the 3' end.
Vector: pCS107; Site 1: EcoRI; Site 2: NotI
Host: Escherichia coli XL1-blue.
Location/Qualifiers
1..643
/organism="Xenopus tropicalis"
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/mol type="mRNA"
/db xref="taxon:8364"
/clone="FB9022122"
/dev stage="egg"
/clone lib="XGC-egg"
/notes="Vector: pCS107; Site 1: EcoRI; Site 2: NotI; cDNA
was oligo dT primed from 5ug of poly A+ RNA from egg.
EcoRI-NotI cut cDNA was then ligated into pCS107 with
EcoRI at the 5' end and NotI at the 3' end"

ORIGIN
Query Match      8.1%; Score 95.8; DB 1; Length 643;
Best Local Similarity 55.1%; Pred. No. 5.4e-17;
Matches 234; Conservative 0; Mismatches 182; Indels 9; Gaps 2;

QY 193 GGTGTCATCTCCATTCCTCTGTATACATCCCTCACACGCTGTTT---AACTGGAAATTTTGA 249
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 83 GGTGATTCGTGATCCCACTCTATATCCCTATGTGCTGACTGGCCAGTGAAGTTTGG 142

QY 250 AGTGGAACTCGATGTTTGGCTCATTAAGTACTATCTTTTGTGCAAGATCGGCTAC 309
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 143 AAAGGCTTGTGAAGTTGTGGTAGTAATGGACTACCTTTTATGCACTGCTTCAGTTTTT 202

QY 310 AGTATTGCTCATTAAGTACTAGTACGATACAGTCAGTTCACACGCTGTCGTTATAGA 369
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DB 203 AATATTGCTCATCACTATGACAGGTTTCTTCAGTCACTAAAGCGGTGCTCTACAGA 262

QY 370 GCACAGCACACTGGCATCTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGGATCTGGCT 429
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 263 GCACAGAAAGAAATGACAAAGAAATGCAGTGTAAATATGCTATTGTTGGTGGCAGCC 322

QY 430 TTCTTGCTCAATGGCCCAATGATTCCTGGCTCGGA-----TTCTTGAAGAACAGACCC 483
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 323 TTTCTTCTATGCGCCAGCCATCATCCCTGGGAATACATTCGAAGAACTACTATCTTA 382

QY 484 AACACAGAGAGTGGAGCTGGCTTTGTTACTGAGTGTACATCTCCGCCATTTACAGCA 543
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 383 CCAGAGGGGAATGTTATGTAGAAATCTACTACAACTGGTATTTTCTGATGATAGCTTCC 442

QY 544 TTCTTGAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCAGTGTACAGATTTACTGG 603
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 443 ACAATAGAAATTTTACTTCCATTCATCAGTGTACCTATTTCAATCTAAGCATCTACATT 502

QY 604 AGCT 608
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DB 503 AACAT 507

RESULT 9
CN423054
LOCUS
DEFINITION
CN423054
VERSION
CN423054.1 GI:47410648
KEYWORDS
EST.
SOURCE
Homo sapiens (human)
ORGANISM
Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
Brandenberger, R., Wei, H., Zhang, S., Lei, S., Murage, J., Fisk, G.J.,
Li, Y., Xu, C., Fang, R., Guegler, K., Rao, M.S., Mandalam, R.,
Lebkowski, J. and Stanton, L.W.
Transcriptome characterization elucidates signaling networks that
control human ES cell growth and differentiation
Nat. Biotechnol. 22 (6), 707-716 (2004)
Contact: Brandenberger R
Regenerative Medicine
Geron Corporation
230 Constitution Drive, Menlo Park, CA 94025, USA
Tel: 650 473 8658
Fax: 650 473 7760

Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00.
Location/Qualifiers
1..716
/organism="Homo sapiens"
/mol type="mRNA"
/db xref="taxon:9606"
/tissue_type="embryonic stem cells, cell lines H1, H7, and
H9"
/clone_lib="GRN ES"
/notes="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

FEATURES
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1..716
Email: rbrandenberger@geron.com
Insert Length: 716 Std Error: 0.00.
Location/Qualifiers
1..716
/organism="Homo sapiens"
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H9"
/clone_lib="GRN ES"
/notes="oligo dT primed, full-length enriched cDNA library
from undifferentiated hES cell lines H1 (p32), H7 (p29),
and H9 (p26) maintained in feeder-free conditions"

ORIGIN
Query Match      8.0%; Score 93.8; DB 7; Length 716;
Best Local Similarity 53.9%; Pred. No. 2.3e-16;
Matches 241; Conservative 0; Mismatches 197; Indels 9; Gaps 2;

QY 192 GGTGTCATCTCCATTCCTCTGTATACATCCCTCACACGCTG---TTTAACTGGAAATTTGG 248
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 200 GGGCGCTTCTGTCATCCCACTGTATGATACCTACGCTGACAGGCGCTGGACCTTCGG 259

QY 249 AAGTGAATCTGCATGTTTGGCTCATTAAGTACTATCTTTTGTGACACATCCGCTA 308
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 260 CCGGGGCTCTGCAAGCTGTGGCTGTAGTGGACTACCTGCTGTGACCTCTCTGCTT 319

QY 309 CAGTATTGCTCTATTAGCTACGATACGATACCACTAGTTCAGTTTCAAAAGCTGTGCGTTATAG 368
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 320 CAACATCGTGTCTCATCAGCTACGACCGTTCTCTGCTGCTCACCAGCGGTCTCATACCG 379

QY 369 AGCACAGCACACTGGCATCTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGGTACTGGC 428
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 380 GGGCCAGCAGGGTGACACGCGCGGCGAGTGCAGAAAGATGCTGCTGTGGGTGGTGGC 439

QY 429 TTTCTTGGTCAATGGCCCAATGATCTGGCTTCGGA-----TTCTTGAAGAACACAGCAC 482
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 440 CTTCTGCTGTAGGACCAACGCTCTGAGTGGAGTACCTGTCGGGGGCGAGCTCAT 499

QY 483 CAACACAGAGAGTGGAGCTGGCTTGTGTTTGTAGTGTGATCATCTCCGCCATTAACAGC 542
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 500 CCCCGAGGGCCACTGCTATGCCAGTTCCTTCAACACTGGTACTTCTCTCATCAGGCTTC 559

QY 543 ATTCTTGAATTCCTGCTCCCTGCTCTCTGTTGGTGTCTATTTCAGTGTACAGATTTACTG 602
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DB 560 CACCTTGGAGTTCTTTACGCCCTTCTCAGCGTACCTTCTTTAACTCAGCATCTACCT 619

QY 603 GAGCTGTGGAAGCTGGGAGTCTCAG 629
    ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| ||| |||
DB 620 GAACATCCAGAGGGGACCCCGCTCCG 646

RESULT 10
BF567596
LOCUS
DEFINITION
BF567596
VERSION
BF567596.1 GI:11677326
KEYWORDS
EST.
SOURCE
Rattus norvegicus (Norway rat)
ORGANISM
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
1 (bases 1 to 499)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to facilitate gene
discovery
Genome Res. 6 (9), 791-806 (1996)
JOURNAL
MEDLINE
PUBMED
8889548
COMMENT
Contact: Soares, MB

```

## Coordinated Laboratory for Computational Genomics

University of Iowa  
375 Newton Road, 4156 MEBRF, Iowa City, IA 52242, USA  
Tel: 319 335 8250  
Fax: 319 335 9565

Email: bento-soares@uiowa.edu  
cDNA Library Preparation: M.B. Soares Lab Clone Distribution:  
clones will be available through Research Genetics (www.resgen.com)  
This clone is also available through the I.M.A.G.E. Consortium at  
LNL (info@image.lnl.gov). IMAGE ID= 1796445  
Seq primer: M13 Forward.

## FEATURES

Location/Qualifiers

source

1..499  
/organism="Rattus norvegicus"  
/mol\_type="mRNA"  
/strain="Sprague-Dawley"  
/db\_xref="taxon:10116"  
/clones="UI-R-B00-agr-c-06-0-UI"  
/dev\_stage="adult"  
/lab\_host="DH10B (Life Technologies)"  
/clone\_lib="UI-R-B00"  
/note="Vector: p773D-Pac (Pharmacia) with a modified  
polylinker; Site 1: Not I; Site 2: Eco RI; The library  
(UI-R-B00) is a subtracted library derived from a mixture  
of the following tissues: thalamus, cerebellum,  
hypothalamus, medulla, pons, midbrain, cerebral cortex,  
corpus striatum and hippocampus. For a detailed  
description of the library from which this clone was  
derived, please visit our web site at  
rategest.eng.uiowa.edu. The subtraction has been previously  
described in (Bonaldo, Lennon and Soares, Genome Research  
6:791-806, 1996)"

## ORIGIN

Query Match 7.7%; Score 90.4; DB 2; Length 499;  
Best Local Similarity 53.8%; Pred. No. 2.1e-15;  
Matches 234; Conservative 0; Mismatches 192; Indels 9; Gaps 2;

Qy 192 GGGTGTCTCATCTCCATCTCTGTACATCCCTCACACGCTGTTTAAAC---TGGAAATTTGG 248  
Db 58 GGGTGCCTTCGCATCCCATTTGATGACCTATGCTGACCGCGCTTGGACCTTCGG 117  
Qy 249 AAGTGGATCTGCATGTTTGGCTCATCTACTGACTATCTTTTGGCAGACATCGTCTA 308  
Db 118 CCGGGGCTCTGCAAGCTGTGGCTGGTGGTAGACTACTGTGTGCTCTCTCGTCTT 177  
Qy 309 CAGTATTGCTCTATTAGTACGATCGATACCATCCAGTTCAGTTTCAAACGCTGTGCGTTATAG 368  
Db 178 CAACATGCTACTATCAGCTATGACCGATTCTGTGCTACTGAGCTGTCTCTACAG 237  
Qy 369 AGCAGACACTGGCATCTCTGAAATTTGTTGCTCAAAATGGTGGCTGTTTGGATATGCG 428  
Db 238 GGCCAGCAGGGGACAGCAGCGGGCGTTTCGGAAGATGCACTGTGTGGTGGCTGGC 297  
Qy 429 TTTCTTGGTCAATGGCCCAATGATTCTGGCTTCGGA-----TTCCTTGAAGAAGACAGC 482  
Db 298 CTTCTCTGTGTATGGGCTGCGCATCTGAGTTGGGAGTACCTGTCTGGTGGCAGTTCCAT 357  
Qy 483 CAACACAGAGAGTGGCGCTGCTTGTGTACTGAGTGGTACATCTCTCGCCATTACAGC 542  
Db 358 CCCCAGGGCCACTGTGATGCTGAGTCTTTCTTCAACTGGTGTACTTCTCATCGGNGTC 417  
Qy 543 ATTCTTGAATTCCTGTCTCTCTGCTCTCTTCTGGTGGTCTATTTCAGTGTACAGATTTACTG 602  
Db 418 CACCCTCGAGTCTTTCAGGCCCTTCTCAGCGTTTACCTTCTTCAACCTCAGCATCTACCT 477  
Qy 603 GAGCTGTGGAGCG 617  
Db 478 GAACATCCAGAGCG 492

## RESULT 11

CNS03296/c

LOCUS CNS03296 921 bp DNA linear GSS 01-SEP-2000  
DEFINITION Tetraodon nigroviridis genome survey sequence T7 end of clone  
206D09 of library G from Tetraodon nigroviridis, genomic survey  
sequence.  
ACCESSION AL224547.1 GI:7883412  
VERSION AL224547.1  
KEYWORDS GSS; genome survey sequence.  
SOURCE Tetraodon nigroviridis  
ORGANISM Tetraodon nigroviridis  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Actinopterygii; Neopterygii; Teleostei; Euteleostei; Neoteleostei;  
Acanthomorpha; Acanthopterygii; Percomorpha; Tetraodontiformes;  
Tetraodontoidea; Tetraodontidae; Tetraodon.  
REFERENCE 1  
AUTHORS Roest Crolius H., Jaillon O., Dasilva C., Bouneau L., Fisher C.,  
Bernot A., Fizames C., Wincker P., Brottier P., Quetier P.,  
Saurin W. and Weissenbach J.  
TITLE Estimate of human gene number provided by genome-wide analysis  
using Tetraodon nigroviridis DNA sequence  
JOURNAL Nat. Genet. 25 (2), 235-238 (2000)  
MEDLINE 20296633  
PUBMED 10835645  
REFERENCE 2  
AUTHORS Roest Crolius H., Jaillon O., Dasilva C., Ozouf-Costaz C.,  
Fizames C., Fischer C., Bouneau L., Billault A., Quetier P.,  
Saurin W., Bernot A. and Weissenbach J.  
TITLE Characterization and repeat analysis of the compact genome of the  
freshwater pufferfish Tetraodon nigroviridis  
JOURNAL Genome Res. 10 (7), 939-949 (2000)  
MEDLINE 20359837  
PUBMED 10899143  
REFERENCE 3 (bases 1 to 921)  
AUTHORS Direct Submission  
TITLE Genoscope.  
JOURNAL Submitted (12-APR-2000) Genoscope - Centre National de Sequencage :  
BP 191 91006 EVRY cedex - FRANCE (E-mail : seque@genoscope.cns.fr  
- web : www.genoscope.cns.fr)  
COMMENT This sequence is a single read and was generated as part of a large  
scale clone-end sequencing project of the Tetraodon nigroviridis  
genome. For more information, please take a look at  
http://www.genoscope.cns.fr/tetraodon.  
FEATURES  
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Query Match 7.6%; Score 89.2; DB 9; Length 921;  
Best Local Similarity 59.4%; Pred. No. 6e-15;  
Matches 171; Conservative 0; Mismatches 113; Indels 4; Gaps 1;  
Qy 889 CTTCTCAGAGCAGGAAGTAGCCAGGTGCGTCTAGCTGCTCTGAGTGTCTTTGCCATT 948  
Db 588 CTGTCCAGAGACAAAAGATTGCCAAATCTCTGCCATTATCGTCTGTATTTTCGGGATC 529  
Qy 949 TGCTGGGCTCGTATTGCTGTTTCAAAATTTGTTTCAACTTATCGCAGGAGGAGCGC 1008  
Db 528 TGCTGGGCCCCCTACACGCTGCTGATGATCATCCGCGCGCTGCGAGGAGTGCCTGG 469  
Qy 1009 CCCAAATTCGATTTGGTACAGCATAGCTTTTGGCTACAGTGTGTTCAATTCCTATTAAAT 1068  
Db 468 CCGACTAC----TGTACGAGATTAACCTTCTGGCTCTCTGGCTCAACTAGCATCAAC 413  
Qy 1069 CCCTTCTATACCTTTGTGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGATCTCTGT 1128  
Db 412 CCCTTCTGTACCGCTGTGCCACAGCAGCTTCCGAGGGCTTTCTCAAGATCCTGTGT 353  
Qy 1129 GTGCAAAAGCAACAGCACCTTTCACAGACCCAGTCAGTATCTTCTTGA 1176

Db 352 CCCAAAGACAGTCGGTTCCAGCCTCAGATCGAAGTCAGTCGGTTAA 305

## RESULT 12

BQ950659

LOCUS

DEFINITION BQ950659 1046 bp mRNA linear EST 21-AUG-2002  
AGENCOURT\_8863943 NIH\_MGC\_129 Mus musculus cDNA clone IMAGE:6311932

5', mRNA sequence.

ACCESSION

BQ950659

VERSION

BQ950659.1 GI:22366137

SOURCE

Mus musculus (house mouse)

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

1 (bases 1 to 1046)  
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Euthera; Chordata; Craniata; Vertebrata; Euteleostomi;  
National Institutes of Health, Mammalian Gene Collection (MGC)  
Unpublished (1999)  
Contact: Robert Strausberg, Ph.D.  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: Susan L. Sullivan, Ph.D.  
cDNA Library Preparation: ResGen, Invitrogen Corp  
cDNA Library Arrayed by: The I.M.A.G.E. Consortium  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: L1AM13736 row: k column: 05  
High quality sequence stop: 640.

## FEATURES

source

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/clone\_lib="NIH\_MGC\_129"  
/note="Organ: olfactory epithelium; Vector: pCMV-SPORT6.1;  
Site 1: EcoRV; Site 2: NotI; Cloned unidirectionally.  
Primer: Oligo dt. Average insert size 2.2 kb. Constructed  
by ResGen, Invitrogen Corp. Note: this is a NIH\_MGC  
Library."

## ORIGIN

Query Match 7.2%; Score 84.2; DB 5; Length 1046;  
Best Local Similarity 56.5%; Pred. No. 2e-13;  
Matches 177; Conservative 0; Mismatches 133; Indels 3; Gaps 1;  
Qy 191 TGGGTGTCATCTCATCTCTGTACATCCCTCACAGCTGTTTAACTGGAATTTTG 247  
Db 438 TAGGTGCTTCTGTGATCCCATTTGATGCTATGCTGACCGCGGTGGACCTTTG 497  
Qy 248 GAAGTGAATCTGATGTTTGGCTCATCTACTACTATCTTTGTGCACAGCATCCGCTCT 307  
Db 498 GCCGGGCTCTGCAAGCTGTGGTGTGTAGTACTACTGCTGTGCTCTCTCATCTCT 557  
Qy 308 ACAGTATGTCCTCATTTAGTACGATCGATACACAGTCAGTTTCAACGCTGTGCGTTATA 367  
Db 558 TCAACATCGTCTGATCAGCTATGACCGGATTCCTGTGTCAGTCACCTCGACTACC 617  
Qy 368 GAGCAGCAGCAGCTGGATCCTGAAATTTGCTCAAAATGGTGGCTGTTGGTATCTGG 427  
Db 618 GGGCCCCAGAGGGGGACACAGAGCGGCTGTTCGAAAGATGGCACTGGTGGGTGCTGG 677  
Qy 428 CTTTCTTGGTCAATGGGCCCAATGATCTTGGCTTCGGATTTCTTGAAGAACAGCACCACCA 487  
Db 678 CTTTCTTGGTCAATGGGCCCTGGCATCTGATTTGGGAGTACCTCTCCGGTGGCACTCCA 737  
Qy 488 CAGAGGAGTGGGA 500  
Db 738 TCCCGAGGGGCCA 750

## RESULT 13

BC019470

LOCUS

DEFINITION

ACCESSION

BC019470

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

COMMENT

REMARK

COMMENT

FEATURES

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1..1136

/organism="Mus musculus"

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/db\_xref="taxon:10090"

/clone="IMAGE:4036375"

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/tissue\_type="Mammary tumor. WAP-TGF alpha model. 7 months

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/tissue\_type="Mammary tumor. WAP-TGF alpha model. 7 months

/tissue\_type="Mammary tumor. WAP-TGF alpha model. 7 months

old, gross tissue."  
 /clone lib="NCI CGAP Mam5"  
 /lab host="DH10B"  
 /note="Vector: pCMV-SPORT6"

## ORIGIN

Query Match 7.0%; Score 82.2; DB 3; Length 1136;  
 Best Local Similarity 56.3%; Pred. No. 8.3e-13;  
 Matches 175; Conservative 0; Mismatches 133; Indels 3; Gaps 1;

QY 73 CTTCCTTTTGCATACGATAGGAATGCTGTGCTGCTATTTAGCTTTGTAGCAGACAGA 132  
 DB |||||  
 QY 568 CTAGCTGTGTGACCATCTATTTGGACATCTTAGCTCATGTTTCCATTAAGTCAACCGC 627  
 DB |||||  
 QY 133 AACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGACTTCTTCGTG 192  
 DB |||||  
 QY 628 CACCTTCAGAGCTGTCAACAATTAATCTTCTTGTTCAGCGCTGGCTGTGCTCATCATCA 687  
 DB |||||  
 QY 193 GGTGTCATCTCCATCTCTGTGATCATCTCTGACAGCTGTTT---AAGTGAATTTTGGGA 249  
 DB |||||  
 QY 688 GGTGTTTTCTCCATGAACATTTGTATACCTCTACACTGTGATTTGGCTACTGGCCCTTTGGGA 747  
 DB |||||  
 QY 250 AGTGAATCTGCATGTTTGGCTCATTAAGTCAATCTTTTGTGACAGCATCGTCTAC 309  
 DB |||||  
 QY 748 CCTGTAGTGTGCGACCTTTGGCTAGCTGATGTTGTGACAAATGCTCCGTTATG 807  
 DB |||||  
 QY 310 AGTATTTCTCTCATTAGCTAGCATGATACAGTCAAGTTCAGGCTGTCGTTATAGA 369  
 DB |||||  
 QY 808 AATCTTCTCATCATCAGCTTTGTATAGATCTTCTGTGTCACAAACCTCTAACCTACCCA 867  
 DB |||||  
 QY 370 GCACAGCACAC 380  
 DB |||||  
 QY 868 GTTAAGCGGAC 878

## RESULT 14

BQ837058  
 LOCUS  
 DEFINITION rf37e04.y1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5', similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ;, mRNA sequence.

ACCESSION BQ837058

VERSION BQ837058.1

KEYWORDS GI:22141376

SOURCE Meloidogyne hapla

ORGANISM Meloidogyne hapla

REFERENCE Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

AUTHORS

1 (bases 1 to 505)  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Teagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP

TITLE

JOURNAL

COMMENT

The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu  
 This clone will not be made available due to an unidentified microbial contamination of the source material.

Seq primer: -40RP from Gibco

High quality sequence step: 407.

FEATURES

source

1. 505

/organism="Meloidogyne hapla"

/mol\_type="mRNA"

/db\_xref="taxon:6305"

/dev\_stage="J2"  
 /lab host="DH10B"

/clone lib="Meloidogyne hapla J2 pAMP1 v1"

/note="Vector: pAMP1 (Gibco); Site 1: Muri; Site 2: SalI;  
 The library was constructed by Claire Murphy and Dr. James McCarter at Washington University, St. Louis. The cDNA was made by using Dynabead oligo-dT priming (Dynal). PCR based library using a modified protocol from the SMART PCR cDNA Synthesis Kit from Clontech. Directionally cloned into the UDG sites of pAMP1. J2 were provided by Dr. Valerie Williamson of the University of California at Davis (vwilliamson@ucdavis.edu)."

## ORIGIN

Query Match 6.8%; Score 79.8; DB 5; Length 505;  
 Best Local Similarity 56.0%; Pred. No. 3.3e-12;  
 Matches 172; Conservative 0; Mismatches 132; Indels 3; Gaps 1;

QY 77 CTTTGTCTATAACGATAGGAATGCTGTGCTATTTAGCTTTGTAGCAGACAGAACC 136  
 DB |||||  
 QY 45 CATTAGCTACAACGATCGGAATGCTCTTGTATGCTTTCTATTGTGTGATAAAAAT 104  
 DB |||||  
 QY 137 TTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCTGACTTCTTCGTGGTG 196  
 DB |||||  
 QY 105 TACAACAATTAGCAATATTTTCTTCTCTTAGCTGTGCTGATCTTACTATTTGGC 164  
 DB |||||  
 QY 197 TCATCTCCATCTCTGTACATCCCTCACACGCTGTTT---AAGTGAATTTTGGAGTG 253  
 DB |||||  
 QY 165 TTATTTCTATCTCTTATGTTCTATATACGCAATGAGACTTTGGTATT 224  
 DB |||||  
 QY 254 GAATCTCATGTTTGGCTCATTAAGTCAATCTTTTGTGACAGCATCTCTACAGTA 313  
 DB |||||  
 QY 225 CTCTTTGTCAATCTGCTCTGTATAGATTTAATGTGCAATGCTTCAGCACTCAAT 284  
 DB |||||  
 QY 314 TTGTCTCATTAGCTAGCATGATACAGTCAAGTTCAGGCTGCTGGTTATAGACAC 373  
 DB |||||  
 QY 285 TGTATTAAATAGCTTTGTATAGATCTTTTCTGTACCCGACCTTAACCTACAGGCCA 344  
 DB |||||  
 QY 374 AGCACAC 380  
 DB |||||  
 QY 345 AGAGAAC 351

## RESULT 15

BQ836551

LOCUS

DEFINITION

rf47c11.y1 Meloidogyne hapla J2 pAMP1 v1 Meloidogyne hapla cDNA 5', similar to TR:Q9XW31 Q9XW31 Y40H4A.1 PROTEIN. [1] ;, mRNA sequence.

ACCESSION BQ836551

VERSION BQ836551.1

KEYWORDS GI:22140865

SOURCE Meloidogyne hapla

ORGANISM Meloidogyne hapla

Eukaryota; Metazoa; Nematoda; Chromadorea; Tylenchida; Tylenchina; Tylenchoidea; Heteroderidae; Meloidogyninae; Meloidogyne.

REFERENCE

AUTHORS

1 (bases 1 to 410)  
 McCarter, J., Clifton, S., Chiapelli, B., Pape, D., Martin, J., Wylie, T., Dante, M., Marra, M., Hillier, L., Kucaba, T., Theising, B., Bowers, Y., Gibbons, M., Ritter, E., Bennett, J., Franklin, C., Teagareishvili, R., Ronko, I., Kennedy, S., Maguire, L., Beck, C., Underwood, K., Steptoe, M., Allen, M., Person, B., Swaller, T., Harvey, N., Schurk, R., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.  
 The Washington Univ. Nematode EST Project, 1999  
 Unpublished (1999)  
 Contact: McCarter JP

TITLE

JOURNAL

COMMENT

The Washington Univ. Nematode EST Project, 1999  
 Washington University School of Medicine  
 4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA  
 Tel: 314 286 1800  
 Fax: 314 286 1810

Email: est@watson.wustl.edu

This clone will not be made available due to an unidentified

microbial contamination of the source material.

Seq primer: -4ORP from Gibco.

Location/Qualifiers

FEATURES

source

1. .410  
/organism="Meloiodogone hapla"  
/mol\_type="mRNA"  
/db\_xref="taxon:6305"  
/dev\_stage="J2"  
/lab\_host="DH10B"  
/clone\_lib="Meloiodogone hapla J2 pAMP1 v1"  
/notes="Vector: pAMP1 (Gibco); Site 1: NotI; Site 2: SalI;  
The library was constructed by Claire Murphy and Dr. James  
McCartney at Washington University, St. Louis. The cDNA was  
made by using Dynabead oligo-dT priming (Dyna). PCR based  
library using a modified protocol from the SMART PCR cDNA  
Synthesis Kit from Clontech. Directionally cloned into the  
UDG sites of pAMP1. J2 were provided by Dr. Valerie  
Williamson of the University of California at Davis  
(vmwilliamson@ucdavis.edu)."

ORIGIN

Query Match 6.6%; Score 78.2; DB 5; Length 410;  
Best Local Similarity 55.7%; Pred. No. 9.3e-12;  
Matches 171; Conservative 0; Mismatches 133; Indels 3; Gaps 1;  
QY 77 CTTTTCGTATAGCAATGCAATGCTGGTCTATTTTAGCCTTTGTAGCAGACAGAAACC 136  
Db |||||  
45 CATTAGCTACAGATCGGAATGCTCTTGTATGCTTTCTATTTGTGTGATAAAAAAT 104  
QY 137 TTAGACATCGAAGTAATTTATTTTCTTAAATTTGGCTATTTCTGACTTCTCGTGGGTG 196  
Db |||||  
105 TACAACAATTAGCAATTTATTTCTTTCTTTTAGCTGTGCTGATCTTACTATTGGGC 164  
QY 197 TCATCTCCATTCCTGTGTACATCCCTCACAGCTGTTT---AAGTGAATTTTGGAGTG 253  
Db |||||  
165 TTATTTCTATTCCTCTTATGACTTTATATACGGCAATGAGACTTGGACTTTTGGTTATT 224  
QY 254 GAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGTGCACAGCATCGTCTACAGTA 313  
Db |||||  
225 CTCTTTGTCAATTCGGCTCTGTATAGATTTATTAATGTGCAATGCTTTCAGCACTCAATT 284  
QY 314 TTGTCCTCATTAGCTACGATCGATACCAGTCAGTTCAGTTTCAAAACGGCTGTGCGTTATAGAGCAC 373  
Db |||||  
285 TGTATTAAATTAGCTTTGTAGATACCTTTTCTGTACCCGACCTTTAACTTACAGGCCAA 344  
QY 374 AGCACAC 380  
Db |||||  
345 AGAGAAC 351

Search completed: August 5, 2005, 14:55:23

Job time : 3701 secs



GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:34:46 ; Search time 165 Seconds  
(without alignments)  
916.505 Million cell updates/sec

Title: US-10-626-126-9  
Perfect score: 2045  
Sequence: 1 M5ENSGTDLPLTAQVPLAF.....WKILCVTKQPAPSQTSQSVSS 391

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 2105692 seqs, 386760381 residues

Total number of hits satisfying chosen parameters: 2105692

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : A\_Geneseq\_16Dec04:.\*  
1: geneseqp1980s:.\*  
2: geneseqp1990s:.\*  
3: geneseqp2000s:.\*  
4: geneseqp2001s:.\*  
5: geneseqp2002s:.\*  
6: geneseqp2003as:.\*  
7: geneseqp2003bs:.\*  
8: geneseqp2004s:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	99.5	391	5	AAM50566 Rat hist
2	1742	85.2	391	5	AAM50565 Mouse his
3	1742	85.2	391	8	ADO29497 Mouse Gpc
4	1403.5	68.6	390	3	AAB02831 Human G p
5	1403.5	68.6	390	3	AAV71297 Human Gp
6	1403.5	68.6	390	4	AAB62445 Human GPC
7	1403.5	68.6	390	4	AAG64477 Human G p
8	1403.5	68.6	390	4	AAAB73622 Human G p
9	1403.5	68.6	390	5	AAM53050 Human G p
10	1403.5	68.6	390	5	ABP98629 Human his
11	1403.5	68.6	390	5	ABB78276 Amino aci
12	1403.5	68.6	390	5	AAM50564 Human his
13	1403.5	68.6	390	5	AAG66023 Human his
14	1403.5	68.6	390	5	AAU74906 Amino aci
15	1403.5	68.6	390	6	ABU92265 Human G-p
16	1403.5	68.6	390	6	ABP81727 Human his
17	1403.5	68.6	390	6	AAE36417 Human H4
18	1403.5	68.6	390	7	ADG98760 Human Gp
19	1403.5	68.6	390	7	ADJ26923 Human end
20	1403.5	68.6	390	8	ADG86375 Human his
21	1403.5	68.6	390	8	ADG86375 Human end
22	1403.5	68.6	390	8	ADJ88376 Novel hum
23	1403.5	68.6	390	8	ADQ05720 Human his
24	1403.5	68.6	390	8	ADO29496 Human GPC
25	1403.5	68.6	390	8	ADP20168 Human G p

26	1403.5	68.6	390	8	ADQ75074 Human G p
27	1403.5	68.6	391	5	AAM53052 Human G p
28	1403.5	68.6	392	5	AAM53053 Human G p
29	1398.5	68.4	390	4	AAM51410 Human GPR
30	1398.5	68.4	390	6	AAE36416 Human H4
31	1398.5	68.4	390	8	ADG86522 Human end
32	1237.5	60.3	389	5	AAM50567 Guinea pi
33	1233	60.3	357	6	AAE36415 Human H4
34	1117.5	54.6	336	6	AAE36414 Human H4
35	698	34.1	445	6	ABR43668 Monkey hi
36	698	34.1	445	6	ABP57426 Monkey hi
37	698	34.1	445	8	ADP76111 Monkey H3
38	693	33.9	445	2	AAW92975 Human mAC
39	693	33.9	445	2	AAAY06322 Human G p
40	693	33.9	445	2	AAAG67830 Human mus
41	693	33.9	445	3	AAAY92218 Human his
42	693	33.9	445	4	AAAB30627 A human h
43	693	33.9	445	5	ABB79792 Human his
44	693	33.9	445	6	ABR43667 Human his
45	693	33.9	445	6	ABP57425 Human his

ALIGNMENTS

RESULT 1  
AAM50566  
ID AAM50566 standard; protein; 391 AA.  
XX  
AC AAM50566;  
XX  
DT 18-MAR-2002 (first entry)  
XX  
DE Rat histamine H4 receptor.  
XX  
KW Histamine H4 receptor; rat; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiac; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.  
XX  
OS Rattus rattus.  
XX  
PN WO200192485-A1.  
XX  
PD 06-DEC-2001.  
XX  
PF 22-FEB-2001; 2001WO-US005914.  
XX  
PR 31-MAY-2000; 2000US-0208260P.  
XX  
PA (ORTH ) ORTHO-MCNEIL PHARM INC.  
XX  
PI Lovenberg T, Liu C;  
XX  
DR WPI; 2002-114339/15.  
DR N-PSDB; AAI70982.  
XX  
New mammalian histamine H4 receptor proteins and polynucleotides encoding the proteins, useful in gene therapy for treating diseases where it is beneficial to elevate mammalian histamine H4 receptor activity.  
XX  
Claim 13; Fig 6A; 92pp; English.  
XX  
The present sequence is that of a rat histamine receptor of the H4 subtype, as predicted from a cDNA clone isolated from a spleen cDNA library. The invention provides mammalian (human, mouse, rat and guinea pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and polypeptides (see AAM50564-67). The nucleic acids have been expressed in recombinant host cells that produce active recombinant protein. The pharmacology of known histamine ligands is demonstrated. Mammalian histamine H4 receptor may be used in gene therapy for the treatment of diseases where it is beneficial to elevate mammalian histamine H4 receptor activity. Recombinant protein is useful for identifying modulators of the histamine H4 receptor. Such modulators may be useful

CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity  
XX  
SQ Sequence 391 AA;

Query Match 99.5%; Score 2034; DB 5; Length 391;  
Best Local Similarity 99.7%; Pred. No. 2.3e-203;  
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;  
Qy 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVILAFVADNLRHRSNYFFLNLAIS 60  
Db 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVILAFVADNLRHRSNYFFLNLAIS 60  
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Db 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
Qy 121 RYRAQHTGILKIQAQVAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
Db 121 RYRAQHTGILKIQAQVAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
Qy 181 AFLEFLLPVSLVYVFSVQIYWSLWKGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
Db 181 AFLEFLLPVSLVYVFSVQIYWSLWKGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
Qy 241 PGLKEPAASLHSESPPKSSLLVSLRTHMGSIIAPKVGFCSRSESPVLHQREHVELLRG 300  
Db 241 PGLKEPAASLHSESPPKSSLLVSLRTHMGSIIAPKVGFCSRSESPVLHQREHVELLRG 300  
Qy 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
Db 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
Qy 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391  
Db 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391

RESULT 2  
AAMS0565  
ID AAMS0565 standard; protein; 391 AA.

XX  
AC AAMS0565;

XX 18-MAR-2002 (first entry)

XX Mouse histamine H4 receptor.

XX Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
KW diagnosis; gene therapy.

XX Mus musculus.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.

XX N-PSDB; AAI70981.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
PT the proteins, useful in gene therapy for treating diseases where it is

PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 13; Fig 5B; 92pp; English.

XX The present sequence is that of a mouse histamine receptor of the H4  
CC subtype, as predicted from a cDNA clone isolated from a spleen cDNA  
CC library. The invention provides mammalian (human, mouse, rat and guinea  
CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
CC polypeptides (see AAMS0564-67). The nucleic acids have been expressed in  
CC recombinant host cells that produce active recombinant protein. The  
CC pharmacology of known histamine ligands is demonstrated. Mammalian  
CC histamine H4 receptor may be used in gene therapy for the treatment of  
CC diseases where it is beneficial to elevate mammalian histamine H4  
CC receptor activity. Recombinant protein is useful for identifying  
CC modulators of the histamine H4 receptor. Such modulators may be useful  
CC for diagnosing, treating or preventing asthma, allergy, inflammation,  
CC cardiovascular and cerebrovascular disorders, non-insulin dependent  
CC diabetes mellitus, hyperglycemia, constipation, arrhythmia, disorders of  
CC the neuroendocrine system, stress and spasticity

XX Sequence 391 AA;

Query Match 85.2%; Score 1742; DB 5; Length 391;  
Best Local Similarity 84.9%; Pred. No. 7.5e-173;  
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVILAFVADNLRHRSNYFFLNLAIS 60  
Db 1 MSESNGTDVLPPLTAQVPLAFMLSLAPAITIGNAVILAFVADNLRHRSNYFFLNLAIS 60  
Qy 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
Db 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVNAV 120  
Qy 121 RYRAQHTGILKIQAQVAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
Db 121 RYRAQHTGILKIQAQVAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180  
Qy 181 AFLEFLLPVSLVYVFSVQIYWSLWKGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
Db 181 AFLEFLLPVSLVYVFSVQIYWSLWKGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
Qy 241 PGLKEPAASLHSESPPKSSLLVSLRTHMGSIIAPKVGFCSRSESPVLHQREHVELLRG 300  
Db 241 PGLKEPAASLHSESPPKSSLLVSLRTHMGSIIAPKVGFCSRSESPVLHQREHVELLRG 300  
Qy 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
Db 301 RKLARSIAVLLSAPAIQWAPCYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360  
Qy 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391  
Db 361 PLCHRRFQKAPFKILCVTKQAPSPQTSVSS 391

RESULT 3  
ADO29497

ID ADO29497 standard; protein; 391 AA.

XX  
AC ADO29497;

XX 29-JUL-2004 (first entry)

XX Mouse GPCR HH4, SEQ ID NO:599.

XX G protein-coupled receptor; GPCR; drug screening; diagnosis;  
KW transgenic mouse; neurological disorder; adrenal gland disorder;  
KW colon disorder; intestinal disorder; cardiovascular disorder;  
KW muscular disorder; blood disorder; immune disorder; bone disorder;  
KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
KW kidney disorder; liver disorder; lung disorder; breast disorder;  
KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;

KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
KW cystostatic; antiinflammatory; vasotropic; antianginal; antiarrhythmic;  
KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
KW virucide; hepatotropic; antibacterial; antianaemic; antiseborrhoeic;  
KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
KW murine; receptor.  
XX Mus musculus.  
XX WO2004040000-A2.  
XX 13-MAY-2004.  
XX 09-SEP-2003; 2003WO-US028226.  
XX 09-SEP-2002; 2002US-0409303P.  
XX 09-APR-2003; 2003US-0461329P.  
XX (PRIM-) PRIMAL INC.  
XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
XX Madisen L, Mcilwain KL, Pavlova MN, Vassilatis D, Zeng H;  
XX WPI; 2004-390329/36.  
XX N-PSDB; ADO30257.  
XX Novel mammalian G protein coupled receptors, useful for identifying  
XX compounds that modulates diagnosing and treating disease condition  
XX associated with GPCR dysfunction e.g. autoimmune diseases, angina  
XX pectoris, Parkinson's disease.  
XX Claim 151; SEQ ID NO 599; 542pp; English.  
XX The invention relates to human and mouse G protein-coupled receptors  
XX (GPCRs) and nucleic acids encoding them. The invention also relates to  
XX sequences at least 90% identical to the GPCR proteins and nucleic acids  
XX of the invention; methods of treating, preventing or diagnosing diseases  
XX associated with GPCRs of the invention; methods of screening for  
XX compounds useful in the treatment of GPCR-related diseases; a transgenic  
XX mouse comprising a GPCR gene of the invention; a mouse comprising a  
XX mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
XX from the transgenic mice; kits comprising several mice, each of which has  
XX a mutation in a different GPCR gene of the invention; and kits comprising  
XX probes which hybridise to GPCR polynucleotides of the invention. The  
XX invention further discloses variants of the GPCR polypeptides and vectors  
XX comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
XX be used in the diagnosis, treatment or prevention of a wide variety of  
XX diseases including neurological disorders (e.g., Alzheimer's disease,  
XX depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
XX disorders of the adrenal gland; disorders of the colon or intestine  
XX (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
XX syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
XX myocardial infarction); muscular disorders; blood disorders (e.g.,  
XX anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
XX AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
XX arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
XX obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
XX diseases); and disorders of the kidney, liver, lung, breast, ovary,  
XX uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
XX thyroid (e.g., cancers). The present sequence represents a GPCR of the  
XX invention. Note: The full sequence data for this patent did not form part  
XX of the printed specification; those sequences not shown were obtained in  
XX electronic format directly from WIPO at  
XX ftp.wipo.int/pub/published\_pcr\_sequences.  
XX Sequence 391 AA;  
XX Query Match 85.2%; Score 1742; DB 8; Length 391;  
XX Best Local Similarity 84.9%; Pred. No. 7.5e-173;  
XX Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;  
OY 1 MSENSTGTLPPAQVPLAFMLSSFAFAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60

Db 1 MSENSTGTLPPAQVPLAFMLSSFAFAIMVGNVAVILAFVVDRLNLRHSNYFFLNLAIS 60  
OY 61 DFFVGVTSIPLYIPIHTLFWNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVSNV 120  
Db 61 DFLVGLSIPLYIPIHTLFWNNPGSGICMFWLITDYLCTASVYSIVLISYDRYQSVSNV 120  
OY 121 RYRAQHTGILKIVAQMVAVILAFVNGPMLASDSWKNSTNTCECEPGFVTEWYLAIT 180  
Db 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLASDSWKNSTNTKDCPEGFVTEWYLAIT 180  
OY 181 AFLEFLIPVSLVYVSQIYHSLMKRGSLSRCPHAGSIATSSRGTGHSRRRTGLACRTSL 240  
Db 181 MLEBFLIPVSVAYFNVQIYWSLWKRRLSRCPHAGSFSTSSASGHLHAGVACRTSN 240  
OY 241 PGLKEPAASLHSESPRGKSSLLVSLRTHMSGIITAFKVGSCFRCSESPVLHOREHVLELRG 300  
Db 241 PGLKESAASRHSSESPRRKSSILVSLRTHMNSITAFKVGSEFWRSESAALRQREYALELRG 300  
OY 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFY 360  
Db 301 RKLARSLAILLSAFAICWAPYCLFTIVLSTYRTERPKSVWYSIAFWLQWNSFVNPFY 360  
OY 361 PLCHRRFOKAFAWKILCVTKQPAPSQTSVSS 391  
Db 361 PLCHRRFOKAFAWKILCVTKQPALSQNSVSS 391  
RESULT 4  
AAB02831  
ID AAB02831 standard; protein; 390 AA.  
XX AC AAB02831;  
XX DT 22-AUG-2000 (first entry)  
XX DE Human G protein coupled receptor hRUP7 protein SEQ ID NO:14.  
XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor;  
XX identification; agonist; screening; therapeutic; pharmaceutical; mutant.  
XX OS Homo sapiens.  
XX PN WO2000022131-A2.  
XX PD 20-APR-2000.  
XX PF 13-OCT-1999; 99WO-US024065.  
XX PR 13-OCT-1998; 98US-00170496.  
XX PR 12-NOV-1998; 98US-0108029P.  
XX PR 20-NOV-1998; 98US-0109213P.  
XX PR 27-NOV-1998; 98US-0110060P.  
XX PR 16-FEB-1999; 99US-0120416P.  
XX PR 26-FEB-1999; 99US-0121852P.  
XX PR 12-MAR-1999; 99US-0123944P.  
XX PR 12-MAR-1999; 99US-0123945P.  
XX PR 12-MAR-1999; 99US-0123946P.  
XX PR 12-MAR-1999; 99US-0123948P.  
XX PR 12-MAR-1999; 99US-0123949P.  
XX PR 12-MAR-1999; 99US-0123951P.  
XX PR 28-MAY-1999; 99US-0136436P.  
XX PR 28-MAY-1999; 99US-0136437P.  
XX PR 28-MAY-1999; 99US-0136439P.  
XX PR 28-MAY-1999; 99US-0137127P.  
XX PR 28-MAY-1999; 99US-0137131P.  
XX PR 28-MAY-1999; 99US-0137567P.  
XX PR 29-JUN-1999; 99US-0141448P.  
XX PR 27-AUG-1999; 99US-0151114P.  
XX PR 03-SEP-1999; 99US-0152524P.  
XX PR 29-SEP-1999; 99US-0156555P.  
XX PR 29-SEP-1999; 99US-0156633P.  
XX PR 29-SEP-1999; 99US-0156634P.



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Db 1 MPTNSTINLSLSTRVTLAFAFMSLVAFAMLGNALVILAFVVDKRLHRSSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFFNMNPGSGICMFMLITDYLCTASVYSIVLISYDRYOSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFMLTTDYLCTASVYVNLISYDRYLSVSNV 120
Qy 121 RYRAQHTGILKIVAQMAVWILAFVNGPMTLASDSWKNSNTTBECEPGFVTEWYLAIT 180
Db 121 SYRTQHTGVLKIVTLMAVWVLAFLVNGPMTLVSESWKDEGS--ECEPGFSEWYLAIT 178
Qy 181 AFLEFLLPVSLVAVVFSQIYVSLWKRGSLRCPHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVIPVLVAFNMNIYWSLWKRDHLSCQHPGLTAVSSNICGHSFGRLSRRSL 238
Qy 241 PGLKEPAASLHSESPRGKSLLSVLRTHMSGIIAFKVGSCRSFSPVLHOREHVLLRG 300
Db 239 SASTEVPAFHSERQRKSSLMFSSRTKMSNTTASKMGFSQSDSVALHQHVELLRA 298
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLFQWNSFVNPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSQ-TOSVSS 391
Db 359 PLCHRRFQKAFKIFCKIKKQPLPSQHSRVS 390

RESULT 6
AAB62445
ID AAB62445 standard; protein; 390 AA.
XX AC AAB62445;
XX DT 09-JUL-2001 (first entry)
XX DE Human GPCR-like polypeptide, PFI-013.
XX KW G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiasthmatic;
XX KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytostatic; human;
XX KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;
XX KW signal transduction.
XX OS Homo sapiens.
XX FN EP1096009-A1.
XX PD 02-MAY-2001.
XX PF 24-OCT-2000; 2000EP-00309364.
XX PR 29-OCT-1999; 99GB-00025641.
XX PR 20-APR-2000; 2000GB-00009973.
XX PA (PFI2 ) PFIZER LTD.
XX PA (PFI2 ) PFIZER INC.
XX PI Peter B, O'reilly MA;
XX DR WPI; 2001-309854/33.
XX DR N-PSDB; AAF83203.
XX PT New G-protein coupled receptor-like polypeptide, polynucleotide for
XX PT screening drug candidates for treating diseases associated with signal
XX PT transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX PS Claim 22; Page 44; 66pp; English.
XX This is a human G-protein coupled receptor (GPCR)-like polypeptide, PFI-
CC 013, encoded by cDNA of NCIMB 41073. The PFI-013 protein can be expressed
CC by standard recombinant methodology. Antibodies and modulators of PFI-013
CC are useful in the manufacture of a medicament for treating allergic
CC disorder, including intrinsic asthma, immunological disorders, such as
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CC intrinsic asthma, vasculitic granulomatous disease, interstitial and
CC other pulmonary disease, including chronic obstructive pulmonary disease
CC (COPD), infectious, inflammatory disease, such as inflammatory bowel
CC disease and neoplastic and myeloproliferative diseases. They are also
CC useful for treating obesity, diabetes, metabolic, neurological diseases,
CC psychotherapeutics, urogenital disease, reproduction and sexual medicine,
CC inflammation, cancer, tissue repair, dermatology, photogeing, skin
CC pigmentation, osteoporosis, cardiovascular, gastrointestinal diseases,
CC allergy and respiratory disease, sensory organ disorders, sleep disorders
CC and hair loss. The PFI-013 protein and nucleic acid are useful in the
CC diagnosis and treatment of the above conditions and also for screening
CC drug candidates for the treatment of diseases associated with signal
CC transduction. The antibodies are also useful for enrichment of
CC eosinophils from mammalian, especially human blood and for detecting the
CC protein in biological samples
XX SQ Sequence 390 AA;
XX Query Match 68.6%; Score 1403.5; DB 4; Length 390;
XX Best Local Similarity 69.1%; Pred. No. 1.7e-137;
XX Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;
Qy 1 MSESNGTDVLPDLTAQVPLAFLMSLLAFAITTGNVAVILAFVADNRLHRSSYFFLNLAIS 60
Db 1 MPTNSTINLSLSTRVTLAFAFMSLVAFAMLGNALVILAFVVDKRLHRSSYFFLNLAIS 60
Qy 61 DFFVGVISIPLYIPHTLFFNMNPGSGICMFMLITDYLCTASVYSIVLISYDRYOSVSNV 120
Db 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFMLTTDYLCTASVYVNLISYDRYLSVSNV 120
Qy 121 RYRAQHTGILKIVAQMAVWILAFVNGPMTLASDSWKNSNTTBECEPGFVTEWYLAIT 180
Db 121 SYRTQHTGVLKIVTLMAVWVLAFLVNGPMTLVSESWKDEGS--ECEPGFSEWYLAIT 178
Qy 181 AFLEFLLPVSLVAVVFSQIYVSLWKRGSLRCPHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVIPVLVAFNMNIYWSLWKRDHLSCQHPGLTAVSSNICGHSFGRLSRRSL 238
Qy 241 PGLKEPAASLHSESPRGKSLLSVLRTHMSGIIAFKVGSCRSFSPVLHOREHVLLRG 300
Db 239 SASTEVPAFHSERQRKSSLMFSSRTKMSNTTASKMGFSQSDSVALHQHVELLRA 298
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLINPLY 360
Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLFQWNSFVNPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQAPSQ-TOSVSS 391
Db 359 PLCHRRFQKAFKIFCKIKKQPLPSQHSRVS 390

RESULT 7
AAG64477
ID AAG64477 standard; protein; 390 AA.
XX AC AAG64477;
XX DT 25-SEP-2001 (first entry)
XX DE Human G protein-coupled receptor protein BG26.
XX KW Human; G protein-coupled receptor protein BG26; histamine H3; histamine;
XX KW altering intracellular CAMP concentration;
XX KW regulating signal transduction.
XX OS Homo sapiens.
XX FN WO200146414-A1.
XX PD 28-JUN-2001.
XX PF 20-DEC-2000; 2000WO-JP009038.
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PR 20-DEC-1999; 99JP-00361687.  
XX (BANY ) BANYU PHARM CO LTD.  
XX Itadani H, Nakamura T, Tanaka K, Ohta M;  
XX WPI; 2001-441675/47.  
DR N-PSDB; AAH47911.  
XX  
PT G protein-coupled receptor protein BG26, with activity of binding to  
PT histamine and capable of changing intracellular cAMP concentration in  
PT response to its stimulus, applicable as tool in screening ligands or drug  
PT candidates.  
XX  
XX  
XX Claim 1; Page 41-44; 50pp; Japanese.  
XX  
XX The present sequence is that of the human G protein-coupled receptor  
CC protein BG26, which shows significant homology with histamine H3, with  
CC activity of binding to histamine and capable of changing intracellular  
CC cAMP concentration in response to its stimulus. The protein is applicable  
CC as a tool in screening ligands or drug candidates for regulating signal  
CC transduction from such protein and treating diseases associated with its  
CC abnormality  
XX  
SQ Sequence 390 AA;  
Query Match 68.6%; Score 1403.5; DB 4; Length 390;  
Best Local Similarity 69.1%; Pred. No. 1.7e-137;  
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;  
QY 1 MSBSNGTDLPLTAQVPLAFMLSLAFATIGNAVILAFVADNRILHRNYPFLNLAIS 60  
DB 1 MPTNSTINISLSTRVTLAFMSLVAFIMLGNALVILAFVDKILHRSSYFPLNLAIS 60  
QY 61 DFFVGVISIPLYIPTHTLFDWDFGKEICVFWLTDDLLCTASVYVILSYDRYLSVNAV 120  
DB 61 DFFVGVISIPLYIPTHTLFDWDFGKEICVFWLTDDLLCTASVYVILSYDRYLSVNAV 120  
QY 121 RYRAQHTGILKIYVAVWVILAFVNGPMLILASDSWKNSTNTECEPGFVTEHYILAIT 180  
DB 121 SYRTQHTGVILKIVTLVAVWVILAFVNGPMLILVSESWKDEGS--ECPGPFSEHYILAIT 178  
QY 181 AFLEFLPLSVLVVYFVQIYVLSWLRGSLRCPSHAGFIATSSRGTHSRRTGLACRTSL 240  
DB 179 SPLEFVPLVILVAFVNNITWSLWKRDLRCQHPGLTAVSSNICHSFAGRLSSRSL 238  
QY 241 PGLKEPAASLHSESPPKSKSLVSLRTHMSGIITAPKVGFCSRSESPVLHQREHVELRG 300  
DB 239 SASTEVPAFSPHERQRKSLMFSSRTKMSNTIASKMGSPSQSDSVALHQREHVELRA 298  
QY 301 RKLARSLAVLLSAPACWAPCYLFTIVLSTYRGERPKSIWYSTAFWLFQNSLINPFLY 360  
DB 299 RRLAKSLAILGLVFAVCWAPYSLFTIVLSFYSSATGPKSVMYRTAFWLFQNSFVNPFLY 358  
QY 361 PLCHRRFQKAFMKILCVTKOPAPSQ--TOSVSS 391  
DB 359 PLCHRRFQKAFMKILCVTKOPAPSQ--TOSVSS 390  
RESULT 8  
AAB73622  
ID AAB73622 standard; protein; 390 AA.  
XX  
AC AAB73622;  
XX  
XX 10-AUG-2001 (first entry)  
XX  
XX Human G protein-coupled receptor AXOR35.  
XX  
XX AXOR35; human; G protein-coupled receptor; 7TM receptor;  
KW histamine H3 receptor homologue; infection; viral; bacterial; fungal;  
KW protozoan; HIV-1; HIV-2; pain; cancer; diabetes; obesity; anorexia;  
KW protozoan; osteoporosis; asthma; allergy; urinary retention;

KW acute heart failure; hypotension; hypertension; angina pectoris;  
KW myocardial infarction; stroke; ulcer; migraine; vomiting;  
KW psychotic disorder; neurological disorder; anxiety; schizophrenia;  
KW manic depression; bipolar disorder; depression; delirium; dementia;  
KW severe mental retardation; dyskinesia; Parkinson's disease;  
KW Huntington's disease; Gilles de la Tourette's syndrome; lymphocyte;  
KW macrophage; eosinophil; neutrophil; function modulation;  
KW autoimmune disorder; pulmonary disorder; gene therapy; vaccine;  
KW drug screening; signal transduction; transgenic animal; drug discovery.  
OS Homo sapiens.  
PN WO200133221-A1.  
XX  
XX 10-MAY-2001.  
XX  
XX 26-OCT-2000; 2000MO-US029461.  
XX  
XX 02-NOV-1999; 99US-00431898.  
PR 03-FEB-2000; 2000US-00497790.  
XX  
XX (SMIK ) SMITHKLINE BEECHAM PLC.  
PA (SMIK ) SMITHKLINE BEECHAM PLC.  
XX  
XX Aubart KM, Bergema DJ, Fitzgerald LR, Graybill TL, Li X;  
PI Michalovich D, Morrow DM, Zhu Y;  
XX  
DR WPI; 2001-316464/33.  
DR N-PSDB; AAH24007.  
XX  
PT Novel G-protein coupled receptor polypeptide and polynucleotide for  
PT treating cancer, autoimmune, pulmonary, cardiovascular and neurological  
PT disorders and for identifying modulators useful for treating asthma.  
XX  
XX Claim 1; Page 50-51; 54pp; English.  
XX  
XX The invention relates to the human G protein-coupled receptor AXOR35  
CC (AAB73622), to cDNA encoding AXOR35 (AAH24006), and to AXOR35 fragments  
CC and variants. Like all G protein-coupled receptors, AXOR35 has 7 putative  
CC transmembrane domains and is involved in signal transduction. AXOR35 has  
CC homology and structural similarity with G protein-coupled receptors such  
CC as the human histamine H3 receptor. The invention also relates to  
CC expression vectors and host cells comprising AXOR35 DNA, to recombinant  
CC expression of AXOR35, and to an AXOR35-specific antibody. AXOR35 proteins  
CC and nucleotides may be used to treat a wide variety of disorders  
CC including bacterial, fungal, protozoal and viral infections, particularly  
CC HIV-1 or HIV-2 infections; pain; cancer; benign prostatic hypertrophy;  
CC diabetes; obesity; anorexia; bulimia; osteoporosis; asthma; allergies;  
CC urinary retention; acute heart failure; hypotension; hypertension; angina  
CC pectoris; myocardial infarction; stroke; ulcers; migraine; vomiting;  
CC psychotic and neurological disorders such as anxiety, schizophrenia,  
CC manic depression, depression, delirium, dementia, and severe mental  
CC retardation, and dyskinesias, such as Parkinson's disease, Huntington's  
CC disease or Gilles de la Tourette's syndrome. AXOR35 proteins and  
CC nucleotides are useful as vaccines, and AXOR35 proteins, nucleotides and  
CC antibodies may be used in screening compounds for their ability to  
CC modulate AXOR35 activity or expression. Such AXOR35 modulators are  
CC particularly useful for treating asthma, and inhibiting or promoting the  
CC function of lymphocytes, macrophages, eosinophils or neutrophils in  
CC asthmatic lung. AXOR35 proteins, nucleotides and antibodies are also  
CC useful for diagnosing or determining susceptibility of an individual to a  
CC disease via the detection of abnormal levels of protein or mRNA, or via  
CC the detection of mutations in the corresponding gene. AXOR35 proteins are  
CC also useful for inducing an immunological response in a mammal against  
CC the above diseases, and for antibody production. AXOR35 nucleotides are  
CC also useful as diagnostic reagents, in chromosome localisation and tissue  
CC expression studies, and for producing transgenic animals useful in drug  
CC discovery. AXOR35-specific antibodies are useful for purifying the AXOR35  
CC protein or fragments thereof, and are also useful for treating conditions  
CC associated with the expression of the AXOR35 protein. The present  
XX sequence represents human AXOR35  
SQ Sequence 390 AA;

Db 121 SYRQHTGVLLKIVLTVAVVWVLAFLVNGPMLVSESWKDEGS--ECEPGFFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVYVFSVOIYWSLWKRGSLSRCPHAGFIATSSRGTHGSRRTGLACTSL 240

Db 179 SFLEFVLPVILVAYFNWNIYWSLWKRDLHSCQHPGLTAVSSNICGHSFRGLSSRSL 238

Qy 241 PGLKEPAASLHSESPPRGKSSLLVSLRTHMGSIIFKVGFCRSESPVLHQREHVELLRG 300

Db 239 SASTEVPAFPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298

Qy 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQFNSEFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKOPAPSQ-TQSVSS 391

Db 359 PLCHKRFQKAFWKILCVTKOPAPSQ-TQSVSS 390

RESULT 10

ABP98629

ID ABP98629 standard; protein; 390 AA.

XX AC ABP98629;

XX DT 13-JUN-2003 (first entry)

XX DE Human histamine receptor SP9144.

XX KW human; histamine receptor; chromosome 18; anti-inflammatory;

XX KW anti-asthmatic; anti-allergic; dermatological; cerebroprotective; stroke;

XX KW anti-migraine; cardiac; anti-rheumatic; anti-arthritis; antipsoriatic;

XX KW neuroprotective; inflammation; asthma; allergy; atopic dermatitis;

XX KW myocardial infarction; migraine; chronic obstructive pulmonary disease;

XX KW rheumatoid arthritis; multiple sclerosis; inflammatory bowel disease;

XX KW psoriasis; receptor.

XX OS Homo sapiens.

XX PN US6204017-B1.

XX PD 20-MAR-2001.

XX PF 07-OCT-1999; 99US-00414010.

XX PR 07-OCT-1999; 99US-00414010.

XX PS (SCHE ) SCHERING CORP.

XX PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;

XX PI Wang S;

XX DR WPI; 2002-442063/47.

XX DR N-PSDB; ABZ80663.

XX PT New nucleic acid encoding antigenic part of human histamine receptor,

XX PT useful for preparing antibodies, e.g. for treating-histamine related

XX PT disorders.

XX PS Example 1; Col 27-30; 19pp; English.

XX CC This sequence represents the amino acid sequence of a human histamine

XX CC receptor (HR) designated SP9144. The sequence was isolated by searching

XX CC databases with the sequence of known G-coupled protein receptor (GPCR).

XX CC The gene is used for recombinant production of HR and for preparing

XX CC antibodies (Ab). These Ab are used to purify HR by immunoaffinity

XX CC chromatography, in immunoassay of histamine receptor, to identify cDNA

XX CC clones that express the receptor, as antagonist to block binding of

XX CC histamine (for treating any histamine-associated disorder) and to

XX CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR

XX CC protein can be used in the treatment of e.g. inflammation, asthma,

XX CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,

XX CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple

CC scleroderma, inflammatory bowel disease and psoriasis

XX SQ Sequence 390 AA;

Query Match 68.6%; Score 1403.5; DB 5; Length 390;

Best Local Similarity 69.1%; Pred. No. 1.7e-137;

Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSBSNGTDVLPALTAQVPLAFMLSLAFAITIGNAVILAFVADRNLRHRSYFFLNLAIS 60

Db 1 MPDTNSTINLSLSTRVTLAFFMSLVAFIMLGNALVILAFVADRNLRHRSYFFLNLAIS 60

Qy 61 DFFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLCTASVYISVILISYDRYQSVNAV 120

Db 61 DFFVGVISIPLYIPHTLFFNMDFGKEICVFWLITDYLCTASVYISVILISYDRYQSVNAV 120

Qy 121 RYRAQHTGILKIYAVQWAVWILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180

Db 121 SYRQHTGVLLKIVLTVAVVWVLAFLVNGPMLVSESWKDEGS--ECEPGFFSEWYILAIT 178

Qy 181 AFLEFLLPVSLVYVFSVOIYWSLWKRGSLSRCPHAGFIATSSRGTHGSRRTGLACTSL 240

Db 179 SFLEFVLPVILVAYFNWNIYWSLWKRDLHSCQHPGLTAVSSNICGHSFRGLSSRSL 238

Qy 241 PGLKEPAASLHSESPPRGKSSLLVSLRTHMGSIIFKVGFCRSESPVLHQREHVELLRG 300

Db 239 SASTEVPAFPHSERQRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298

Qy 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQFNLSINPFLY 360

Db 299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQFNSEFVNPLLY 358

Qy 361 PLCHRRFQKAFWKILCVTKOPAPSQ-TQSVSS 391

Db 359 PLCHKRFQKAFWKILCVTKOPAPSQ-TQSVSS 390

RESULT 11

ABB78276

ID ABB78276 standard; protein; 390 AA.

XX AC ABB78276;

XX DT 05-DEC-2002 (first entry)

XX DE Amino acid sequence of human histamine receptor.

XX KW Human; histamine receptor; receptor; inflammation; asthma; allergy;

XX KW atopic dermatitis; stroke; myocardial infarction; migraine;

XX KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;

XX KW multiple sclerosis; inflammatory bowel disease; psoriasis;

XX KW intracellular second messenger pathway; cellular growth rate;

XX KW hormone secretion.

XX OS Homo sapiens.

XX PN US2002098539-A1.

XX PD 25-JUL-2002.

XX PF 19-MAR-2001; 2001US-00812216.

XX PR 07-OCT-1999; 99US-00414010.

XX PS (BEHA/) BEHAN J X.

XX PI (HEDR/) HEDRICK J A.

XX PI (LAZT/) LAZ T M.

XX PI (MONS/) MONSMA F J.

XX PI (MORS/) MORSE K L.

XX PI (UMLA/) UMLAND S P.

XX PI (WANG/) WANG S.

XX PI Behan JX, Hedrick JA, Laz TM, Monsma FJ, Morse KL, Umland SP;

```
Query Match      68.6%; Score 1403.5; DB 4; Length 390;
Best Local Similarity 69.1%; Pred. No. 1.7e-137;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

Qy 1 MSEGNGTDVLPPLTAQVPLAFMLSLAFITGNVAVILAFVADNRHRSYFFFLNLAIS 60
Db 1 MPDNTNINSLSTRVTLAPFMSLVAFALMGNALVILAFVVDKNLHRSYFFFLNLAIS 60

Qy 61 DFFVGVISIPLYIPHTLPMNPGSGICMFWLITDYLCTASVYISVLYSDRYQSVNAV 120
Db 61 DFFVGVISIPLYIPHTLPMNPGSGICMFWLITDYLCTASVYISVLYSDRYQSVNAV 120

Qy 121 RYRAQHTGILKIVAQMVAVILAFVNGPMTILADSKNSNTNTECEPGFVTEWYILAIT 180
Db 121 SYRQHTGVLKIVLMAVAVILAFVNGPMTILADSKNSNTNTECEPGFVTEWYILAIT 178

Qy 181 AFLBFLPVSLVYVFSVQIYVMSLWKRGSLSRCPHAGFIATSRGTGHSRRTGLACRTSL 240
Db 179 SFLEFVIPVILVAVFNMIYVMSLWKRDLHSLRCQSHPGGLTAVSSNICGHSFGRLLSRSL 238

Qy 241 PGLPEASLHSESPRGKSSLLVSLRTHMSGSIAPKVGSCRSFSPVLHOREHVELLRG 300
Db 239 SASTEVPAFSEQRKRKSSLMFSRSTKMSNTTASKMGSPFSQSDVALHQREHVELLRA 298

Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTVRRGERPKSIWYSIAFWLQWNSLINPPLY 360
Db 299 RRLAKSLAILLCVAVCPWPSLSLTIIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPPLY 358

Qy 361 PLCHRRFQKAPWKILCVTKQAPSQ-TQSUS 391
Db 359 PLCHRRFQKAPWKILCVTKQAPSQ-TQSUS 390

RESULT 9
ID AAM53050 standard; protein; 390 AA.
AC AAM53050;
XX
XX
XX 26-MAR-2002 (first entry)
XX
XX
XX Human G protein-coupled receptor nGPCR-2067.
DE
DE Human; nGPCR-2067; G protein-coupled receptor; 7TM receptor;
KW signal transduction; mental disorder; central nervous system disease;
KW metabolic disease; infection; HIV-1; HIV-2; pain; neurological disorder;
KW psychotic disorder; Huntington's disease; schizophrenia; migraine;
KW depression; anxiety; bipolar disorder; dementia; Alzheimer's disease;
KW Parkinson's disease; proliferative disorder; cancer; psoriasis;
KW benign prostatic hypertrophy; diabetes; dyslipidemia; obesity; anorexia;
KW thyroid disorder; cardiovascular disease; hypotension; hypertension;
KW thrombosis; myocardial infarction; cardiomyopathy; atherosclerosis;
KW inflammatory conditions; autoimmune disorder; rheumatoid arthritis;
KW hormonal disorder; renal failure; anti-HIV; analgesic; cytostatic;
KW antidiabetic; metabolic; hypertensive; hypotensive; thrombolytic;
KW cardiant; antiatherosclerotic; neuroleptic; antimigraine;
KW antiparkinsonian; tranquiliser; antidepressant; neuroprotective;
KW anticonvulsant; antinflammatory; antirheumatic; antiarthritic;
KW antipsoriatic; gene therapy; receptor.
XX
OS Homo sapiens.
XX
XX
XX Location/Qualifiers
FH 19..41
FT Domain
FT /label= Transmembrane_domain_1
FT 52..74
FT Domain
FT /label= Transmembrane_domain_2
FT 86..110
FT Domain
FT /label= Transmembrane_domain_3
FT 128..146
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FT /label= Transmembrane_domain_4
FT 172..194
FT Domain

/label= Transmembrane_domain_5
305..326
/label= Transmembrane_domain_6
342..360
/label= Transmembrane_domain_7

WO200185793-A2.
15-NOV-2001.
08-MAY-2001; 2001WO-US014750.
08-MAY-2000; 2000US-0203108P.
(PHAA ) PHARMACIA & UPJOHN CO.
Lind P, Sejltitz T, Vogeli G, Wood LS;
WPI; 2002-062240/08.
N-PSDB; ABA02496.

New polynucleotide, useful for identifying modulator compounds which are
used for treating psoriasis, schizophrenia, diabetes, encodes the novel G
protein-coupled receptor (nGPCR) polypeptide (nGPCR-2067).

Claim 31; Page 63; 100pp; English.

This sequence represents a novel human G protein-coupled receptor (GPCR)
designated nGPCR-2067. Like all GPCRs, nGPCR-2067 has 7 putative
transmembrane domains and is involved in signal transduction. The
invention also relates to expression vectors and host cells comprising
nucleic acids encoding nGPCR-2067, to recombinant expression of nGPCR-
2067, to antibodies specific for nGPCR-2067, to drug screening methods
that use nGPCR-2067, and to modulators of nGPCR-2067 activity. nGPCR-2067
nucleic acid sequences may be used to isolate nGPCR-2067 allelic variants
and species homologues and may also be used in genetic mapping. The
invention also discloses the use of nGPCR-2067 nucleic acids in screening
for a predisposition to nGPCR-2067-associated hereditary mental
disorders, or for the diagnosis of these disorders. nGPCR-2067 nucleic
acids may additionally be used to generate transgenic animals, including
knockout animals, which may provide an insight into treating a variety of
human disorders, and may also be used in the design of antisense
molecules for suppressing expression of nGPCR-2067 in cells. nGPCR-2067,
and nGPCR-2067 modulators may be used to treat a wide variety of medical
conditions, particularly mental disorders, central nervous system
diseases, and metabolic diseases. Diseases that may be treated include
viral infections, particularly HIV-1 or HIV-2 infections; pain; central
nervous system, neurological and psychotic disorders such as Huntington's
disease, schizophrenia, migraine, depression, anxiety, bipolar disorder,
dementia, Alzheimer's disease, and Parkinson's disease; proliferative
disorders such as cancers, benign prostatic hypertrophy and psoriasis;
metabolic disorders such as diabetes, dyslipidemia, obesity, and
anorexia; thyroid disorders; cardiovascular diseases such as hypotension,
hypertension, thrombosis, myocardial infarction, cardiomyopathies, and
atherosclerosis; inflammatory conditions; autoimmune disorders (e.g.,
rheumatoid arthritis); hormonal disorders; and renal failure
```







modulators of signal transduction for treating kidney disease, hyperlipidemia, obesity, dyslexia and cardiac myxoma.

Claim 26; Page 61; 78pp; English.

The present invention relates to a new G-protein coupled receptor (GPCR) polypeptide comprising greater than 70% amino acid sequence identity to the amino acid sequence of human GPCRs TGR21, TGR130.1, TGR130.2, human TGR213 or TGR92. 80% amino acid sequence identity to mouse TGR18 or 90% amino acid sequence identity to human novel edg receptor protein, as defined in the specification. The GPCR covalently linked to a solid phase is useful for identifying a compound that modulates signal transduction. The identified compounds are useful for treating kidney disease, cerebral cavernous malformations, hyperlipidemia, obesity, dyslexia and cardiac myxoma. The molecules of the invention are useful for diagnosing disorders or conditions such as kidney-related conditions or diseases such as renal failure, nephritis, nephrotic syndrome, or diseases urinary abnormalities, renal tubule defects, hypertension and nephrolithiasis, liver-related disease or condition e.g. cirrhosis, infiltrations, lesions, functional disorders and jaundice and spleen-associated disorders or conditions e.g. splenic enlargement, immune disorders, blood disorders and others. Modulation of the polypeptide of the invention is useful to treat or prevent any of the above conditions or diseases. The present amino acid sequence represents the human GPCR TGR62 protein of the invention. This sequence is one of seven novel G protein coupled receptors of the invention (AAU74904-AAU74911).



GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:39:17 ; Search time 158 Seconds  
(without alignments)  
964.157 Million cell updates/sec

Title: US-10-626-126-9  
Perfect score: 2045  
Sequence: 1 MSEGNGTDVLPTRAQVPLAF.....WKILCVTKQAPAPQTSQSVSS 391

Scoring table: BLOSUM62

Searched: Gapop 10.0 , Gapext 0.5

Total number of hits satisfying chosen parameters: 1745140 seqs, 389608008 residues

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

- Database : Published Applications AA:\*
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  - 2: /cgn2\_6/ptodata/1/pubpaa/PCT\_NEW\_PUB.pep.\*
  - 3: /cgn2\_6/ptodata/1/pubpaa/US06\_NEW\_PUB.pep.\*
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  - 5: /cgn2\_6/ptodata/1/pubpaa/US07\_NEW\_PUB.pep.\*
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  - 11: /cgn2\_6/ptodata/1/pubpaa/US09C\_PUBCOMB.pep.\*
  - 12: /cgn2\_6/ptodata/1/pubpaa/US09\_NEW\_PUB.pep.\*
  - 13: /cgn2\_6/ptodata/1/pubpaa/US10A\_PUBCOMB.pep.\*
  - 14: /cgn2\_6/ptodata/1/pubpaa/US10B\_PUBCOMB.pep.\*
  - 15: /cgn2\_6/ptodata/1/pubpaa/US10C\_PUBCOMB.pep.\*
  - 16: /cgn2\_6/ptodata/1/pubpaa/US10D\_PUBCOMB.pep.\*
  - 17: /cgn2\_6/ptodata/1/pubpaa/US10E\_PUBCOMB.pep.\*
  - 18: /cgn2\_6/ptodata/1/pubpaa/US10\_NEW\_PUB.pep.\*
  - 19: /cgn2\_6/ptodata/1/pubpaa/US11A\_PUBCOMB.pep.\*
  - 20: /cgn2\_6/ptodata/1/pubpaa/US11\_NEW\_PUB.pep.\*
  - 21: /cgn2\_6/ptodata/1/pubpaa/US60\_NEW\_PUB.pep.\*
  - 22: /cgn2\_6/ptodata/1/pubpaa/US60\_PUBCOMB.pep.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	2045	100.0	391	17	US-10-626-126-9
3	2045	100.0	391	17	US-10-626-398-9
4	1735	84.8	391	16	US-10-626-445-8
5	1735	84.8	391	17	US-10-626-126-8
6	1735	84.8	391	17	US-10-626-398-8
7	1403.5	68.6	390	9	US-09-812-216-2
8	1403.5	68.6	390	9	US-09-910-411-2
9	1403.5	68.6	390	10	US-09-875-076-14
10	1403.5	68.6	390	10	US-09-876-252-14
11	1403.5	68.6	390	10	US-09-852-165-2

12	1403.5	68.6	390	10	US-09-891-138A-6	Sequence 6, Appli
13	1403.5	68.6	390	13	US-10-052-193-2	Sequence 2, Appli
14	1403.5	68.6	390	14	US-10-225-567A-629	Sequence 629, App
15	1403.5	68.6	390	14	US-10-272-983-14	Sequence 14, Appl
16	1403.5	68.6	390	14	US-10-354-769-2	Sequence 2, Appli
17	1403.5	68.6	390	14	US-10-393-807-14	Sequence 14, Appl
18	1403.5	68.6	390	15	US-10-417-820A-14	Sequence 14, Appl
19	1403.5	68.6	390	15	US-10-349-253A-12	Sequence 2, Appli
20	1403.5	68.6	390	16	US-10-696-673-2	Sequence 2, Appli
21	1403.5	68.6	390	16	US-10-723-955-14	Sequence 14, Appl
22	1403.5	68.6	390	16	US-10-782-596-14	Sequence 14, Appl
23	1403.5	68.6	390	16	US-10-737-619-2	Sequence 2, Appli
24	1403.5	68.6	390	16	US-10-626-445-2	Sequence 2, Appli
25	1403.5	68.6	390	17	US-10-684-206-20	Sequence 20, Appl
26	1403.5	68.6	390	17	US-10-616-088-2	Sequence 2, Appli
27	1403.5	68.6	390	17	US-10-626-126-2	Sequence 2, Appli
28	1403.5	68.6	390	17	US-10-626-398-2	Sequence 2, Appli
29	1398.5	68.4	390	14	US-10-290-078-27	Sequence 27, Appl
30	1236.5	60.5	389	16	US-10-626-445-10	Sequence 10, Appl
31	1236.5	60.5	389	17	US-10-626-126-10	Sequence 10, Appl
32	1236.5	60.5	389	17	US-10-626-398-10	Sequence 10, Appl
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35	693	33.9	445	9	US-09-350-206-2	Sequence 2, Appli
36	693	33.9	445	9	US-09-349-755-2	Sequence 2, Appli
37	693	33.9	445	9	US-09-166-334-2	Sequence 2, Appli
38	693	33.9	445	14	US-10-282-958-2	Sequence 2, Appli
39	693	33.9	445	14	US-10-325-567A-549	Sequence 549, App
40	693	33.9	445	15	US-10-453-106-1	Sequence 1, Appli
41	693	33.9	445	16	US-10-727-021-7	Sequence 7, Appli
42	693	33.9	445	16	US-10-757-262-132	Sequence 132, App
43	693	33.9	445	17	US-10-735-963-1	Sequence 1, Appli
44	693	33.9	453	9	US-09-891-053-20	Sequence 20, Appl
45	693	33.9	453	17	US-10-759-463-20	Sequence 20, Appl

ALIGNMENTS

RESULT 1  
US-10-626-445-9  
; Sequence 9, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27  
; SOFTWARE: PatentIn version 3.2  
; SEQ ID NO 9  
; LENGTH: 391  
; TYPE: PRT  
; ORGANISM: Rattus rattus  
; US-10-626-445-9

Query Match	100.0%	Score 2045;	DB 16;	Length 391;
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Db 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180
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Db 241 PGLKEPAASLHSES PRGKSLVSLRTHMGSIIAFKVGSCFCSSES PVLHQREHVELLRG 300
QY 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPPLY 360
Db 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPPLY 360
QY 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391
Db 361 PLCHRRFQKAFWKILCVTKQAPSPQTSQSVSS 391
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## RESULT 2

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US-10-626-126-9
; Sequence 9, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-126-9
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Query Match 100.0%; Score 2045; DB 17; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.1e-183;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPPLY 360
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## RESULT 3

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US-10-626-398-9
; Sequence 9, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 9
; LENGTH: 391
; TYPE: PRT
; ORGANISM: Rattus rattus
US-10-626-398-9
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Query Match 100.0%; Score 2045; DB 17; Length 391;
Best Local Similarity 100.0%; Pred. No. 1.1e-183;
Matches 391; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
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Db 1 MSESNGTDVLP LTAQVPLAFMSLLAFATITGNNAVILAFVADNRLHRNSNYFFLNLAIS 60
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Db 61 DFFVGVISIPLYIPTHLPNNPGSGICMFWLIITDYLLCTASVYISVILSYDQYOSVNAV 120
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Db 121 RYRAQHTGILKIVAQMVAWVILAFVNGPMLASDSWKNSTNTECEPGFVTEWYILAIT 180
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Db 241 PGLKEPAASLHSES PRGKSLVSLRTHMGSIIAFKVGSCFCSSES PVLHQREHVELLRG 300
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Db 301 RKLARSIAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPPLY 360
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US-10-626-445-8
; Sequence 8, Application US/10626445
; Publication No. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
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## RESULT 7

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US-09-812-216-2
; Sequence 2, Application US/09812216
; Publication No. US20020098539A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Jiang Xu
; APPLICANT: Hedrick, Joseph A.
; APPLICANT: Laz, Thomas M.
; APPLICANT: Monsma, Frederick J. Jr.
; APPLICANT: Morse, Kelley L.
; APPLICANT: Umland, Shelby P.
; APPLICANT: Wang, Suke
; TITLE OF INVENTION: Histamine receptor
; FILE REFERENCE: CN01069
; CURRENT APPLICATION NUMBER: US/09/812,216
; CURRENT FILING DATE: 2001-03-19
; PRIOR APPLICATION NUMBER: 09/414,010
; PRIOR FILING DATE: 1999-10-07
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-812-216-2

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Query Match	68.6t;	Score	1403.5;	DB	9;	Length	390;
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Gaps	2;						
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Qy	61	DFPVGVISIPLYIPHTLFFNNPMSGICMFMLITDYLCTASVYGVLSYDRYOSGVNA	120				
Db	61	DFPVGVISIPLYIPHTLFEWDFGKEICVFMLTTDYLCTASVYGVLSYDRYLSGVNA	120				
Qy	121	RYRAQHTGILKIVAQMAVAILAFVNGPMLIASDSWKNSNTNTECPGFVTEVILAIT	180				
Db	121	SYRTQHTGVCLKIVTLMVAVMVLAFVNGPMLIVSESKWDBGS--ECSPGFSEWYILAIT	178				
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Db	179	SFLFVFPVILVAYFNNNIYSLWKRDHLRSCQSHPGILTAVSSNICGHSFGRLLSSRRSL	238				
Qy	241	PGLKEPAASLHSESPPROKSSLLVSLRTHMSGSIITAFKVGSPCRSESPVLHOREHVELLR	300				
Db	239	SASTEVPASPHERQRRKSSLMFSSRRTKMSNTTASQMGFSQSDSVALHOREHVELLRA	298				
Qy	301	RKLARSILAVLLSAPAIWAPYCLFTIVLSTVYRRGERPKSIWYSIAFWLQWPNLSINPPLY	360				
Db	299	RRLAKSLAILLGVAFCWAPYSLFTIVLSFYSSATGPKSVWYRTAFWLOWFNSVPNPPLY	358				
Qy	361	PLCHRRFOKAPFKWILCVTKQPAPSQ--TQSVSS	391				
Db	359	PLCHRRFOKAPFKLFCIKKQPLPQSHRSVSS	390				

## RESULT 8

US-09-910-411-2  
; Sequence 2, Application US/09910411  
; Patent No. US20020137054A1

[illegible]



; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,127
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/137,131
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/141,448
; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,293
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-875-076-14

Query Match 68.6%; Score 1403.5; DB 10; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

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Db 1 MPDNTNINLSLSTRVILAFMSLAFVAFIMLGNALVILAFVVDKRLHRSSYFFFLNLAIS 60

Qy 61 DFFVGVISIPILYIPHTLFFNNPGSGICMFWLITDYLLCTASVYIVLSIDRYOSVSNV 120
Db 61 DFFVGVISIPILYIPHTLFEWDFGKEICVFWLTLDYLLCTASVYIVLSIDRYLSVSNV 120

Qy 121 RYRQHTGILKIVAQVAVWILAFVLNPGMILASDSKWNSTNTECEPGFTWYILAIT 180
Db 121 SYRTQHTGVKLIVTMVAVWILAFVLNPGMILVSNESWKNDEGS--ECEPGFTSEWYILAIT 178

Qy 181 AFLEPFLPVSLVYVFSVOIYWSLWKRGSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
Db 179 SFLEFVIVILVAFNMNIYWSLWKRDLHSLQCQHPGLTAVSSNICGHSFGRLSRRSL 238

Qy 241 PGLKEPAASHSESPRGKSSLLVLRTHMSGIIAFKVGSCFRCSESPVLHQREHVELLRG 300
Db 239 SASTEVPASPFSSRQRKRKSSLMFSSRTKQNSNTIASKGFSQSDSVLHQREHVELLRA 298

Qy 301 RKLARSLAVLSAFAICWAPYCLFTVLVSTRGRERPKSIWYSTAFWLQWNSLNIPPLY 360
Db 301 RKLARSLAVLSAFAICWAPYCLFTVLVSTRGRERPKSIWYSTAFWLQWNSLNIPPLY 360

Db 299 RRLAKSLAILLGVPFVAVCWAPYSLETVILSFVSSATGPKSVWYRIAFWLQWNSFVNPLY 358
Qy 361 PLCHRRFQKAFWKILCVTKQPAPSQ-TQSVSS 391
Db 359 PLCHKRQKAFKIFCIKKQPLPSQHSRSVSS 390

RESULT 10
US-09-876-252-14
; Sequence 14, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Rec
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
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; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
; PRIOR FILING DATE: 1998-11-12
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; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
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; PRIOR FILING DATE: 1999-05-28
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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
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; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653

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; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 14
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-876-252-14

Query Match
Best Local Similarity 68.6%; Score 1403.5; DB 10; Length 390;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSBSNGTDVLPATAQVPLAFMSLLAPAITGNVAVILAFVADRNLRHRSNYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFPMISLVAFIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60
QY 61 DFFVGVISIPLYIPHTLFWNNPGSGICMFWLIIDYLLCTASVYSIVLISYDRYQSVSNV 120
DB 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTIDYLLCTASVYNIVLISYDRYLSVSNV 120
QY 121 RYRAQHTGILKIIVAQVAVWILAFVNGPMLASDSWKNSTNTEECPEGVFTWYILAIT 180
DB 121 SYRTOHTGVLIKIVTLMVAVWVILAFVNGPMLVSESWKDEGS--ECEPGPFSEWYILAIT 178
QY 181 AFLEFLLPVSLVYVFSQIYWSLWKRGSRCPSHAGFIATSSRGTHGSRRTGLACRTSL 240
DB 179 SFLEFVLPVLVAYFNNNIYWSLWKRDLHSCQHPGLTAVSNNICGSPRGLSSRSLS 238
QY 241 PGLKEPAASLHSPRSRKSSLLVSLRTHMSGSIAPKVGSCFCSSESPLVHQREHVELLRG 300
DB 239 SASTEVPAASHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFLY 360
DB 299 RRLAKSLAILLGVFAVCWAPYSUFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPLLY 358
QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ--TQSVSS 391
DB 359 PLCHKRQKAFKIFCIKKQPLFSQHSRSVSS 390

RESULT 12
US-09-891-138A-6
; Sequence 6, Application US/09891138A
; Publication No. US20030083245A1
; GENERAL INFORMATION:
; APPLICANT: Lin, Daniel Chi-Hong
; APPLICANT: Zhao, Jiagang
; APPLICANT: Chen, Jin-Long
; APPLICANT: Cutler, Gene
; APPLICANT: Tularik Inc.
; TITLE OF INVENTION: No. US20030083245A1e1 Receptors
; FILE REFERENCE: 018781-006210US
; CURRENT APPLICATION NUMBER: US/09/891,138A
; CURRENT FILING DATE: 2001-06-25
; PRIOR APPLICATION NUMBER: US 60/213,461
; PRIOR FILING DATE: 2000-06-23
; NUMBER OF SEQ ID NOS: 26
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 6
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
; FEATURE:
; OTHER INFORMATION: human TGR62 G-protein coupled receptor (GPCR)
US-09-891-138A-6

Query Match
Best Local Similarity 68.6%; Score 1403.5; DB 10; Length 390;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSBSNGTDVLPATAQVPLAFMSLLAPAITGNVAVILAFVADRNLRHRSNYFFLNLAIS 60
DB 1 MPDNTNINLSLSTRVTLAFPMISLVAFIMLGNALVILAFVVDKNLRHRSYFFLNLAIS 60
QY 61 DFFVGVISIPLYIPHTLFWNNPGSGICMFWLIIDYLLCTASVYSIVLISYDRYQSVSNV 120
DB 61 DFFVGVISIPLYIPHTLFEWDFGKEICVFWLTIDYLLCTASVYNIVLISYDRYLSVSNV 120
QY 121 RYRAQHTGILKIIVAQVAVWILAFVNGPMLASDSWKNSTNTEECPEGVFTWYILAIT 180
DB 121 SYRTOHTGVLIKIVTLMVAVWVILAFVNGPMLVSESWKDEGS--ECEPGPFSEWYILAIT 178
QY 181 AFLEFLLPVSLVYVFSQIYWSLWKRGSRCPSHAGFIATSSRGTHGSRRTGLACRTSL 240
DB 179 SFLEFVLPVLVAYFNNNIYWSLWKRDLHSCQHPGLTAVSNNICGSPRGLSSRSLS 238
QY 241 PGLKEPAASLHSPRSRKSSLLVSLRTHMSGSIAPKVGSCFCSSESPLVHQREHVELLRG 300
DB 239 SASTEVPAASHSERQRRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQREHVELLRA 298
QY 301 RKLARSLAVLLSAFAICWAPYCLFTIVLSTYRGERPKSIWYSIAFWLQWNSLINPFLY 360
DB 299 RRLAKSLAILLGVFAVCWAPYSUFTIVLSFYSSATGPKSVWYRIAFWLOWFNSFVNPLLY 358
QY 361 PLCHRRFQKAFWKILCVTKOPAPSQ--TQSVSS 391
DB 359 PLCHKRQKAFKIFCIKKQPLFSQHSRSVSS 390

RESULT 11
US-09-852-165-2
; Sequence 2, Application US/09852165
; Publication No. US20030032784A1
; GENERAL INFORMATION:
; APPLICANT: Lind, Peter
; APPLICANT: Sejlitz, Torsten
; APPLICANT: Vogel, Gabriel
; APPLICANT: Wood, Linda S.
; TITLE OF INVENTION: No. US20030032784A1e1 G Protein-Coupled Receptors
; FILE REFERENCE: 00231regUS
; CURRENT APPLICATION NUMBER: US/09/852,165
; CURRENT FILING DATE: 2001-05-08
; PRIOR APPLICATION NUMBER: US98 60/203,108
; PRIOR FILING DATE: 2000-05-08
; NUMBER OF SEQ ID NOS: 3
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens

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Qy	181	AFLEFLLPVSLVWVFSVOIYWSLWKRGSLRCPSHAGFIATSSRGTCGHSRRRTGLACRTSL	240
Db	179	SFLSEFVPIVLVAVFNMMIYWSLWKCRDHLRCQSHPGLTAVSSNICGHSFRCGLSSRSL	238
Qy	241	PGLKEPAASLHSPRGKSSLLVSLRTHMSGSIITAFKVGSPCRSSPVLHQREHVELLRG	300
Db	239	SASTEVPASPHSERQRKRSSLMFSSRTQNGNTIASKMGSPSQSDSVALLHQREHVELLRA	298
Qy	301	RKLARSLAVLLSFAICWAPYCLFTIVLSTYRGRPKSIWYSIAFWLQWNSLNNPFLY	360
Db	299	RRLAKSLAILLCVFAVCWAPYSLFTIVLSTYSSATGPKSVWYRIAPWLQWNSFVNPDL	358
Qy	361	PLCHRRFQKAFWKILCVTKQPAPSQ - TQSVSS	391
Db	359	PLCHRFQKAPLKFICIKOPLPSOHSRSSVSS	390

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RESULT 13
US-10-052-193-2
; Sequence 2, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; CURRENT FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; PRIOR FILING DATE: 2001-01-17
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 2
; LENGTH: 390
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-052-193-2

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RESULT 14
US-10-225
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; PRIOR
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; NUMBER
; SOFTWARE
; SEQ ID
; LENGTH
; TYPE
; ORGAN
US-10-225

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[illegible]

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RESULT 15
US-10-272
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Query Match	68.6%;	Score	1403.5;	DB	13;	Length	390;
Best Local Similarity	69.1%;	Pred. No.	2.6e-123;				
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						Gaps	2;
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Qy	61	DPFVGVISIP	LYIPHTLFNNMPGSGICMFWLITDYLLCTASYSYISVLISYDRYQSVSNV	120			
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Qy	121	RYRAQHTGILK	IVAAQVAVWTLAFLVNGPMLIASDSWKNSNTNTECEGPFVTEWVILAIT	180			
Db	121	SYRTQHTGVLK	IVITLMVAWVLAFLVNGPMLIVSSEWKDEGS--ECEPGPFSEWVILAIT	178			
Qy	181	AFLEFLPVS	LIVVYFVSQIYWSLWKRGSLRCPESHAGFIATSSRGTHSRRTGLACRTSL	240			
Db	179	SFLEFVIV	LVAYFNNMIYWSLWKRDHLRCQSHPGLTAVSSNICGHSFRCRLSSRSL	238			
Qy	241	PGLKEPAASH	UESPRGKSLLVSLRTHMSGSIITAFKVGSPCRSSSPVLHOREHVELLRG	300			
Db	239	SASTEVPASP	FHSERQRKRSSLMFSSRTQWNTTIAASKMGSPSQSDVALHOREHVELLRA	298			
Qy	301	RKLARSALLVS	ASAFICWAPYCLFTVILSTYRRGERPKSIWYSIAFWLQWNSLNPFLY	360			
Db	299	RLAKSLAILL	GVFAVCWAPYSLFTVILSPYSSATGPKSVWYRIAFWLQWNSFVNPLLY	358			
Qy	361	PLCHRRFOK	AFWKILCVTKQAPSQ--TOSVSS	391			
Db	359	PLCHKRFOK	AFKLPICIKKQPLPSQHSRSVSS	390			

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/ PRIOR FILING DATE: 1998-11-20
/ PRIOR APPLICATION NUMBER: 60/120,416
/ PRIOR FILING DATE: 1999-02-16
/ PRIOR APPLICATION NUMBER: 60/121,851
/ PRIOR FILING DATE: 1999-02-26
/ PRIOR APPLICATION NUMBER: 60/123,946
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/123,949
/ PRIOR FILING DATE: 1999-03-12
/ PRIOR APPLICATION NUMBER: 60/136,436
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,437
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,439
/ PRIOR FILING DATE: 1999-05-28
/ PRIOR APPLICATION NUMBER: 60/136,567
/ PRIOR FILING DATE: 1999-05-28
/ Remaining Prior Application data removed - See File Wrapper or PALM.
/ NUMBER OF SEQ ID NOS: 74
/ SOFTWARE: PatentIn Ver. 2.1
/ SEQ ID NO 14
/ LENGTH: 390
/ TYPE: PRT
/ ORGANISM: Homo sapiens
US-10-272-983-14

Query Match      68.6%; Score 1403.5; DB 14; Length 390;
Best Local Similarity 69.1%; Pred. No. 2.6e-123;
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY      1 MBSNGTDVLPVLAQVPLAFMLSLAFATIGNAVILAFVADRNLHRHNSYFFLNLAIS 60
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      1 MPTNSTINLSLSTRTVTLAFPMGLVAFPAIMLGNALVILAFVVDKXNLHRHSSYFFLNLAIS 60
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QY      61 DPFVGVISIPLYIPHTLFFNNPGSGICMFWLITDYLLCTASVYIVLISYDRYQSVNAV 120
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|
Db      61 DPFVGVISIPLYIPHTLFFNDPGKEICVFWLTTDYLLCTASVYIVLISYDRYLSVNAV 120
      |:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|:::|

QY      121 RYRAOHTGILKIYAQVAVWILAFVLNGPMILASDSWKNSTNTECEPGFVTEWYILAIT 180
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Db      121 SYRTQHTGVLIKIVLMAVAVWVLAFLVNGPMILVSESWKDEGS--ECEPGFSEWYILAIT 178
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QY      181 AFLFLLPVSLVYVFSQIYWSLWKRGSLSRCPSHAGFIATSSRGTHSRRTGLACRTSL 240
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QY      241 PGLKEPAASHSESPRGKSLLSLRTHMSGSLIAFKVGSFCRSESVPVLRHSHVELLRG 300
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Db      239 SASTEVPAFSPHSERRKSSLMFSSRTKMSNTIASKMGFSQSDSVALHQRBHVELLRA 298
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QY      301 RKLARSLAVLLSAFACWAPCYCLFTIVLSTYRGERPKSIWYSTAFWLQWNSLINEPLY 360
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Db      299 RRLAKSLAILLGVFAVCWAPYSLFTIVLSFYSSATGPKSVWYRIAFWLQWNSFVNPFLY 358
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QY      361 PLCHRRFQAKFWIKLVTKQAPSQ-TQSVSS 391
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Db      359 PLCHRRFQAKFLKIFCIKKQPLPSQHSRSVSS 390
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Search completed: August 3, 2005, 01:51:12  
Job time : 159 secs

GenCore version 5.1.6  
Copyright (c) 1993 - 2005 CompuGen Ltd.

OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 12:29:04 ; Search time 4456 Seconds

(without alignments)  
4251.793 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSENSTGTVLPLTAQVPLAF.....WKILCVTKQPAPSTQTSVSS 391

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Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 4708233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-DB=GenEmbl -QFMT=fastap -SUPFIX=rge -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCALIGN=200 -THR SCORE=spt -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=spt -NORM=ext -HEAPSIZ=500 -MINLEN=0 -MAXLEN=200000000  
-USER=US10626126 @CGN 1 1 5600 @runat\_02082005\_155436\_2005 -NCPU=6 -ICPU=3  
-NO\_MMAP -LARGQUERY -NEG\_SCORES=0 -WAIT -DSPELOCK=100 -LONGLOG  
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-FGAEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

GenEmbl :

1: gb\_ba:\*  
2: gb\_htg:\*  
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6: gb\_pat:\*  
7: gb\_ph:\*  
8: gb\_pl:\*  
9: gb\_pr:\*  
10: gb\_ro:\*  
11: gb\_ats:\*  
12: gb\_sy:\*  
13: gb\_un:\*  
14: gb\_vi:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
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2	1742	85.2	1538	10 AF358859	AF358859 Mus muscu
3	1434	70.1	23694	2 AC118386	AC118386 Rattus no
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5	1403.5	68.6	1173	6	AR142850	Sequence
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#### ALIGNMENTS

RESULT 1	AF358860	AF358860	1593 bp	mRNA	linear	ROD 02-SEP-2001
LOCUS	AF358860	Rattus norvegicus histamine H4 receptor mRNA, complete cds.				
DEFINITION	AF358860	Rattus norvegicus histamine H4 receptor mRNA, complete cds.				
ACCESSION	AF358860	AF358860.1	GI:15420536			
VERSION	AF358860	AF358860.1	GI:15420536			
KEYWORDS						
SOURCE		Rattus norvegicus (Norway rat)				
ORGANISM		Rattus norvegicus				
REFERENCE		1 (bases 1 to 1593)				
AUTHORS		Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.				
TITLE		Comparison of human, mouse, rat, and guinea pig histamine H4 receptor suggests substantial species variation				
JOURNAL		Unpublished				
REFERENCE		2 (bases 1 to 1593)				
AUTHORS		Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.				
TITLE		Direct Submision				
JOURNAL		Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego, CA 92121, USA				
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ORIGIN
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US-10-626-126-9 (1-391) x AF358860 (1-1593)

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REFERENCE
1 (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
2 (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
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LOCUS
AF358859 1538 bp mRNA linear ROD 02-SEP-2001
DEFINITION Mus musculus histamine H4 receptor mRNA, complete cds.
ACCESSION AF358859
VERSION AF358859.1 GI:15420534
KEYWORDS Mus musculus (house mouse)
ORGANISM Mus musculus
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
REFERENCE
1 (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Comparison of human, mouse, rat, and guinea pig histamine H4
receptor suggests substantial species variation
Unpublished
2 (bases 1 to 1538)
Liu, C., Wilson, S., Kuei, C. and Lovenberg, T.W.
Direct Submission
Submitted (12-MAR-2001) Molecular Pharmacology, The R.W. Johnson
Pharmaceutical Research Institute, 3210 Merryfield Row, San Diego,
CA 92121, USA
LOCATION/Qualifiers
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## ORIGIN

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US-10-626-126-9 (1-391) x AF358859 (1-1538)

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RESULT 3  
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 \*\*\*, 3 unordered pieces.  
 AC118386  
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 SOURCE Rattus norvegicus  
 ORGANISM Rattus norvegicus  
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ACCESSION AY008280.1 GI:15822540
VERSION
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REFERENCE 1 (bases 1 to 1173)
Nguyen,T., Shapiro,D.A., George,S.R., Setola,V., Lee,D.K.,
Cheng,R., Rauser,L., Lee,S.P., Lynch,K.R., Roth,B.L. and
O'Dowd,B.P.
O'Dowd,B.P.
Discovery of a novel member of the histamine receptor family
Mol. Pharmacol. 59 (3), 427-433 (2001)
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PUBMED 11179435
REFERENCE 2 (bases 1 to 1173)
Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.P.
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Discovery of H4, a Novel Histamine Receptor
Unpublished
3 (bases 1 to 1173)
Nguyen,T., George,S.R., Lee,D.K., Cheng,R., Lynch,K.R. and
O'Dowd,B.P.
Direct Submission
Submitted (26-SEP-2000) Pharmacology, University of Toronto, 8
Taddle Creek Rd., Rm. 4353, Toronto, Ont M5S 1A8, Canada
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VSSNICHSPFRSGRLSRSLSTASVEPASPHSRQRKSSLMFSSRTKMNSNTIASKM
GSPSQSSVALHQREHVELLRARLAKSLAILLGVFAVCWAPYSILFIVLSPYSATG
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Alignment Scores:
Pred. No.: 2,096-107 Length: 1173
Score: 1405.50 Matches: 271
Percent Similarity: 79.59% Conservative: 41

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Best Local Similarity: 69.13% Mismatches: 77
Query Match: 68.73% Indels: 3
DB: 9 Gaps: 2
US-10-626-126-9 (1-391) x AY008280 (1-1173)
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Db 1 ATGCAGATACATAATAGCACAAATCAATTTATCATAAGCACTCGTGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAenAlaValAlaIleLeuAlaPhe 40
Db 61 TTTATGCTCTAGTAGCTTTTGTATATATGATGAAATGCTTTGTGCTATTTAGCTTTT 120
Qy 41 ValAlaAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGGCCATCTCT 180
Qy 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTTATGTACACA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTGCTCTCATCAGCTATGATCGATACCTGTCAGTCTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACTCTGGGTCTTGAAGATTGTTACTCTCATGCTGGCCGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCTCTCTTAGTGAATGGCCCAATGATTTCTAGTTTCAGAGCTTTGGAAGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTTGGAAATTCGTGATCCAGTCACTCTAGTGTGCTTATTTTCAACATGAATATTTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCTGTGGAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCTCTGGACTGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCACATCTCTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCTCTGCATCTCTTTCATTCAGAGACACAGAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 775 CTATGTTTTCTCAAGAACCAAGATGAATAGCAATCAATTTGCTTCCAAATGGGTGCC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAATGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTTGTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
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QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAenProPheLeuTyr 360
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QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuValThrLysGln 380
Db 1075 CCATTGTGTCAAGCGCTTCAAAAGGCTTCTTGAANAATATTTTGTATATAAAAGCAA 1134
QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACAAACAGTCGGTCAATCTTCT 1170

RESULT 5
ARI42850
LOCUS ARI42850 1173 bp DNA linear PAT 08-AUG-2001
DEFINITION Sequence 1 from patent US 6204017.
ACCESSION ARI42850
VERSION ARI42850.1 GI:15104136
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITLE Polynucleotide encoding a histamine receptor
JOURNAL Patent: US 6204017-A 1 20-MAR-2001;
FEATURES
Location/Qualifiers
1..1173
source
/organism="unknown"
/mol_type="unassigned DNA"

ORIGIN
Alignment Scores:
Pred. No.: 3.06e-107 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x ARI42850 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACTAATACACCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValAlaIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGAGCTTTTGGTATATATGCTAGAAATGCTTTGGTCAATTTAGCTTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAAGTGGCCATCTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTCTCTTGGGTGTGATCTCCATTCCTTTGATACATCCCTCACGCTGTTTCAATGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGTCTACTACTGATCTGATCTGTTATGTACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTGCTCATCAGCTATGATCGATACCTGTGATCTCAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATCTGGGGTCTTGAAGATTTGTTACTCTGCTGGTGGCGCTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160

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Db 421 GTCTGGCCTTCTTAGTAATGGCCATGATTTCTAGTTTCAGAGTCTTGAAGAGTAA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 534
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCCTTATTTCACATGAATATTAT 594
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGTGGCCAAAGCCATCTCGACTGACTGCT 654
QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAACATCTGTGCACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAAGTTCCTGCATCTCTTCATTCAGAGAGACAGAGAGAAAGAGTAGT 774
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QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACCTGGCCATCTCTTAGGGGTTTTTGTCTGTGTGGCTGCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
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QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAenProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCTCTTTGTAT 1074
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Db 1075 CCATTGTGTCAAGCGCTTCAAAAGGCTTCTTGAANAATATTTTGTATATAAAAGCAA 1134
QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCACACACAGTCGGTCAATCTTCT 1170

RESULT 6
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LOCUS ARI42850 1173 bp DNA linear PAT 18-DEC-2003
DEFINITION Sequence 1 from patent US 6613533.
ACCESSION ARI42850
VERSION ARI42850.1 GI:40115588
KEYWORDS
SOURCE
ORGANISM
Unclassified.
REFERENCE 1 (bases 1 to 1173)
AUTHORS Behan,J.X., Hedrick,J.A., Laz,T.M., Monsma,F.J., Morse,K.L.,
Umland,S.P. and Wang,S.
TITLE Histamine receptor
JOURNAL Patent: US 6613533-A 1 02-SEP-2003;
FEATURES
Location/Qualifiers
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source
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ORIGIN
Alignment Scores:

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Pred. No.: 3 06e-107 Length: 1173  
Score: 1403.50 Matches: 271  
Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AK391860 (1-1173)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
Db 1 ATGCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATT 60  
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Db 61 TTTATGTCCTTAGTAGCTTTTCTATATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120  
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGTGGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTTAACTTGGCCATCTCT 180  
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
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Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
Qy 101 SerValTyrSerIleValIleLeuSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
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Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTyr 140  
Db 361 TCTTATAGAACTCAACATCTGGGGCTTTGAGATTGTTACTCTCATGCTGGCCGTTTGG 420  
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160  
Db 421 GTGCTGGCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGAGTAA 480  
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180  
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAACTGGTACATCTTGGCCATCACA 534  
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
Db 535 TCATCTTGGAAATTCGTGATCCAGTCACTTAGTCGCTTATTTTCAACATGAAATTTAT 594  
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Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
Db 715 TCTGCATCGACAGAAGTTCCTGCATCTCTTTCATTCAGAGACAGAGAGAAAGTAGT 774  
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Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
Db 835 TTCTCCCAATCAGATTTCTGTAGCTCTTCCACAAAGGGAACATGTTGAACATGCTTAGAGCC 894  
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
Db 895 AGGAGATTAGCCCACTGCGCCATCTCTTTAGGGGTTTTTGTCTGTTGCTGGCTCCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
Db 955 TATTCTCTGTTTCACAATTTGCTTTTATTTTATTTTCTCAGCAACAGGCTCTAAATCACTT 1014  
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTyrPheAsnSerLeuIleAsnProPheLeuTyr 360  
Db 1015 TGGTATAGATTGCAATTTGGCTTCAGTGGTTCATTTCTTGTCAATCTCTTTTGTAT 1074  
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
Db 1075 CCATTGTGTCAACAGCGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATATAAAAGCAA 1134  
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
Db 1135 CCTTACCATCACACACAGTCGCTCAGTATCTTCT 1170

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DEFINITION Sequence 1 from Patent WO0125432.  
ACCESSION AX109119  
VERSION AX109119.1 GI:13924093  
KEYWORDS  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
REFERENCE 1  
AUTHORS Behan, J. X., Hedrick, J. A., Laz, T. M., Monema, P. J., Morse, K. L.,  
Umland, S. and Wang, S.  
TITLE Histamine receptor  
JOURNAL Patent: WO 0125432-A 1 12-APR-2001;  
SCHERING CORPORATION (US)  
FEATURES  
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ORIGIN  
Alignment Scores:  
Pred. No.: 3 06e-107 Length: 1173  
Score: 1403.50 Matches: 271  
Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AX109119 (1-1173)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
Db 1 ATGCAGATACATAAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATT 60  
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
Db 61 TTTATGTCCTTAGTAGCTTTTCTATATAATGCTAGGAAATGCTTTGGTCAATTTAGCTTTT 120  
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGTGGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTTAACTTGGCCATCTCT 180  
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGG 240  
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
Db 241 GATTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300  
Qy 101 SerValTyrSerIleValIleLeuSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
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Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
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Qy 141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAepSerTrpLysAenSer 160
Db 421 GTGCTGGCCCTTCTAGTGAATGGCCCAATGATCTAGTTTCAGAGTCTTGGAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr 200
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Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
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Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
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Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSer 260
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Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
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Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTGCTGTGTGGGCTCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCAATGTTCTTTTCAATTTTATTTCTCAGCAACAGGCTCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAlaPheLeuTyr 360
Db 1015 TGGTATAGAATTGCATTTGGCTTTCAGTGGTCAATCTCTTTGTCAATCTCTTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTACAGCCCTTCAAGAGCTTTCTTGAAATATTTTGTATATAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGTGGTCAATCTTCT 1170

RESULT 8
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LOCUS AX139113 1173 bp DNA linear PAT 30-MAY-2001
DEFINITION Sequence 1 from Patent EP1096009.
ACCESSION AX139113
VERSION AX139113.1 GI:14274791
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1
REFERENCE
AUTHORS Peter.B. and O'Reilly.M.A.
TITLE G-protein coupled receptor-like polypeptide
JOURNAL Patent: EP 1096009-A 1 02-MAY-2001;
Pfizer Limited (GB) ; PFIZER INC. (US)

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FEATURES             Location/Qualifiers
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## ORIGIN

## Alignment Scores:

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Pred. No.:          3,06e-107      Length:      1173
Score:              1403.50         Matches:    271
Percent Similarity: 79.34%         Conservative: 40
Best Local Similarity: 69.13%      Mismatches: 78
Query Match:        68.63%         Indels:      3
DB:                 6               Gaps:         2

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US-10-626-126-9 (1-391) x AX139113 (1-1173)

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Qy 41 ValAlaAspArgAenLeuArgHisArgSerAsnTyrPhePheLeuAenLeuAlaIleSer 60
Db 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCTCACAGCTGTTTCAATGG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGATTATTTGGCTCACTACTGACTATCTGTTATGTACGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAenAlaVal 120
Db 301 TCTGTATATAACATTTGCTTCATCAGCTATGATCGATACCTGTCAGTCTCAAAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTATAGAAGCTCAACATCTGGGCTTCAAGATTGTTACTCTGATGGTGGCGTTTGG 420
Qy 141 IleLeuAlaPheLeuValAenGlyProMetIleLeuAlaSerAepSerTrpLysAenSer 160
Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCCAATGATTTCTAGTTTCAGAGTCTTGGAAAGGATGAA 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGCATCACA 534
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGlnIleTyr 200
Db 535 TCATTCTTGAATTCGGATGCCAGTCATCTTAGTCGCTTATTTCACATGAATATTAT 594
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCTCTCAGTAGGTGCCAAGCCATCTCGACTGACTGCT 654
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSer 260
Db 715 TCTGCATCGACAGAGTCTCTGCATCTTTCATTCAGAGAGACAGAGAGAGTAGT 774
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
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Score: 1403.50 Matches: 271
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Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
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ACCESSION AF325356.1 GI:15553202
VERSION
KEYWORDS
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
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REFERENCE 1 (bases 1 to 1173)
AUTHORS Zhu,Y., Michalovich,D., Wu,H.-L., Tan,K.B., Dytko,G.M.,
Mannan,I.J., Boyce,R., Alston,J., Tierney,L.A., Li,X.,
Herrity,N.C., Vawter,L., Sarau,H.M., Ames,R.S., Davenport,C.M.,
Hieble,P., Wilson,S., Bergsma,D.J. and Fitzgerald,L.R.
Cloning, expression, and pharmacological characterization of a
novel human histamine receptor
Mol. Pharmacol. 59 (3), 434-441 (2001)
JOURNAL MEDLINE 21106320
PUBMED 11179436
REFERENCE 2 (bases 1 to 1173)
AUTHORS Zhu,Y., Michalovich,D. and Fitzgerald,L.R.
Direct Submission
TITLE Submitted (30-NOV-2000) GlaxoSmithKline, 709 Swedeland Rd., PO Box
1539, King of Prussia, PA 19406, USA
JOURNAL
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Best Local Similarity:	69.13%	Mismatches:	78
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DB:	9	Gaps:	2

US-10-626-126-9 (1-391) x AF325356 (1-1173)

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LOCUS Homo sapiens histamine receptor H4 mRNA, complete cds.

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ACCESSION AF329449

VERSION AF329449.1 GI:13876643

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ORGANISM Homo sapiens

REFERENCE 1 (bases 1 to 1173)

AUTHORS Morse, K.L., Behan, J., Laz, T.M., West, R.E. Jr., Greenfeder, S.A., Anthes, J.C., Umland, S., Wan, Y., Hipkin, R.W., Gonsiorek, W., Shin, N., Gustafson, E.L., Qiao, X., Wang, S., Hedrick, J.A., Greene, J., Bayne, M. and Monsma, F.J. Jr.

TITLE Cloning and characterization of a novel human histamine receptor

JOURNAL J. Pharmacol. Exp. Ther. 296 (3), 1058-1066 (2001)

MEDLINE 21104636

PUBMED 11181941

REFERENCE 2 (bases 1 to 1173)

AUTHORS Monsma, F.J. Jr., Wang, S., Behan, J., Laz, T.M., Greene, J. and Bayne, M.

TITLE Direct Submission

JOURNAL Submitted (15-DEC-2000) Human Genomics Research, Schering-Plough Research Institute, 2015 Galloping Hill Rd., Kenilworth, NJ 07033, USA

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ACCESSION AJ298292.1 GI:18152452  
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1  
AUTHORS O'Reilly, M.A.  
TITLE Identification of a histamine H4 receptor on human eosinophils -  
Role in eosinophil chemotaxis  
JOURNAL Unpublished  
AUTHORS 2 (bases 1 to 1173)  
O'Reilly, M.A.  
TITLE Direct Submission  
JOURNAL Submitted (11-JAN-2001) O'Reilly M.A., Discovery Biology, Pfizer  
Ltd, Ramsgate Road, Sandwich, Kent, CT13 9NJ, UNITED KINGDOM  
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Qy     241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
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Db     715 TCTGCATCGACAGAAGTTCCTGCATCTCTTTCATTTCAGAGACAGAGAGAGAGTAGT 774
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Qy     261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280
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Db     775 CTCATGTTTTCTTCAAGAACCAAGATGAATAGCAATACAAATTGCTTCCAAAATGGGTTC 834
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Qy     281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
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Db     835 TTCTCCCAATCAGATCTCTAGTCTTTCACAAAGGGAACATGTTGAATGCTTAGAGCC 894
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Qy     301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
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Db     895 AGGAGATTAGCCAAGTCACCTGGCCATTCTCTAGGGGTTTTTGTGCTGTGGCTGCCA 954
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Qy     321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
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Db     955 TATTCTCTGTTCACAATTGCTCTTTCATTTTATTCTCTCAGCAACAGGTCCTAAATCAGTT 1014
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Qy     341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
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Db     1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCTCTTTTGTAT 1074
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Qy     361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
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Db     1075 CCATTGTGTCAACAGCGCTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAAGCAA 1134
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Qy     381 ProAlaProSerGln---ThrGlnSerValSerSer 391
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Db     1135 CCTCTACCATCACAAACACAGTCGGTCAGTATCTTCT 1170
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 12:17:55 ; Search time 573 Seconds

(without alignments)  
4039.474 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 M5ESNGTDVLPITQAQVPLAF.....WKILCVTKQAPASQTSQSVSS 391

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Searched: 4390206 seqs, 2959870667 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Command line parameters:

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-FGAPEXT=7 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

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2: Geneseqn1990s:\*  
3: Geneseqn2000s:\*  
4: Geneseqn2001as:\*  
5: Geneseqn2001bs:\*  
6: Geneseqn2002as:\*  
7: Geneseqn2002bs:\*  
8: Geneseqn2003as:\*  
9: Geneseqn2003bs:\*  
10: Geneseqn2003cs:\*  
11: Geneseqn2003ds:\*  
12: Geneseqn2004as:\*  
13: Geneseqn2004bs:\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	2034	99.5	1176	6	Aai70982 Rat hist
2	1742	85.2	1176	6	Aai70981 Mouse his
3	1742	85.2	1538	12	Ado30257 Mouse GPC
4	1403.5	68.6	1170	9	Aad55126 Human H4
5	1403.5	68.6	1173	3	Aaa46023 Human G p

6	1403.5	68.6	1173	3	AAD01124	Aad01124 Human orp
7	1403.5	68.6	1173	4	AAF83203	Aaf83203 Human GPC
8	1403.5	68.6	1173	5	Aah24007	Aah24007 Human G p
9	1403.5	68.6	1173	6	ABz80663	Abz80663 Human his
10	1403.5	68.6	1173	6	ABQ78739	Abq78739 Nucleotid
11	1403.5	68.6	1173	6	AAI70980	Aai70980 Human his
12	1403.5	68.6	1173	6	AAI67750	Aai67750 Human his
13	1403.5	68.6	1173	8	ACA93262	ACA93262 Human cdn
14	1403.5	68.6	1173	10	ADG98759	Adg98759 Human orp
15	1403.5	68.6	1173	10	ABs57063	ABs57063 Human cdn
16	1403.5	68.6	1173	11	ADJ26922	Adj26922 Human end
17	1403.5	68.6	1173	12	ADG86374	Adg86374 Human end
18	1403.5	68.6	1173	12	ADJ88375	Adj88375 Novel hum
19	1403.5	68.6	1173	12	ADP20167	Adp20167 Human G p
20	1403.5	68.6	1173	12	ADQ75073	Adq75073 Human cdn
21	1403.5	68.6	1266	6	ABK12959	Abk12959 DNA seque
22	1403.5	68.6	1300	6	ABA02496	Abao2496 Human G p
23	1403.5	68.6	1312	4	Aah47911	Aah47911 Human G p
24	1403.5	68.6	3689	8	ABZ42573	Abz42573 Human his
25	1403.5	68.6	3689	12	ADO05719	Ado05719 Human his
26	1403.5	68.6	3689	12	ADO29967	Ado29967 Human GPC
27	1398.5	68.4	1227	4	AAI66009	Aai66009 Human GPR
28	1398.5	68.4	1265	6	AAI598078	Aai598078 Human DNA
29	1398.5	68.4	1265	9	AAI55125	Aai55125 Human H4
30	1237.5	60.5	1170	6	AAI70983	Aai70983 Guinea pi
31	1233	60.3	1166	9	AAI55124	Aai55124 Human H4
32	1117.5	54.6	1103	9	AAI44573	Aai44573 Human mus
33	693	33.9	1334	2	AAI44573	Aai44573 Human mus
34	693	33.9	1335	2	AAI44573	Aai44573 Human mus
35	693	33.9	1335	3	AAI44573	Aai44573 Human mus
36	693	33.9	1335	4	AAI44573	Aai44573 Human mus
37	693	33.9	1335	9	AAI44573	Aai44573 Human mus
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39	693	33.9	1335	13	AAI44573	Aai44573 Human mus
40	693	33.9	1338	12	AAI44573	Aai44573 Human mus
41	693	33.9	1401	9	AAI44573	Aai44573 Human mus
42	693	33.9	2050	2	AAI44573	Aai44573 Human mus
43	693	33.9	2050	3	AAI44573	Aai44573 Human mus
44	693	33.9	2689	2	AAI44573	Aai44573 Human mus
45	693	33.9	2689	2	AAI44573	Aai44573 Human mus

#### ALIGNMENTS

RESULT 1

AAI70982  
ID AAI70982 standard; cdna; 1176 BP.

AC AAI70982;

DT 18-MAR-2002 (first entry)

DE Rat histamine H4 receptor cdna.

XX Histamine H4 receptor; rat; antiaesthetic; antiallergenic;  
XX antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
XX diagnosis; gene therapy; ss.  
XX Rattus rattus.

XX WO200192485-A1.

XX 06-DEC-2001.

XX 22-FEB-2001; 2001WO-US005914.

XX 31-MAY-2000; 2000US-0208260P.

XX (ORTH ) ORTHO-MCNEIL PHARM INC.

XX Lovenberg T, Liu C;

XX WPI; 2002-114339/15.

DR P-P8DB; AAM50566.  
 XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.  
 XX  
 XX  
 PS Claim 4; Fig 5C; 92pp; English.  
 PS  
 CC The present sequence is that of a cDNA clone encoding a rat histamine  
 CC receptor of the H4 subtype. The cDNA was isolated from a rat spleen cDNA  
 CC library. It shows 72.5% homology to the human H4 receptor coding region.  
 CC The invention provides mammalian (human, mouse, rat and guinea pig)  
 CC histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity  
 XX  
 SQ Sequence 1176 BP; 260 A; 293 C; 270 G; 353 T; 0 U; 0 Other;

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 Query Match: 99.46% Indels: 0  
 Ds: 6 Gaps: 0

US-10-626-126-9 (1-391) x AAI70982 (1-1176)

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 QY 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 DB 61 TTAATGTCCTGCTTGTCTTGTATACGATCGAAGTAATATTTTCTTAAATTTGGCTATT 120  
 QY 41 ValAlaAspAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATATTTTCTTAAATTTGGCTATTCT 180  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
 DB 181 GACTTCTTCTGGGTGTATCTCCATCTCTGTATCCCTCCACACGCTGTTTAACTGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 AATTTTGGAGTGAATCTGCATGTTTGGCTCAITTACTGACTATCTTTGTGCGACAGCA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCCGTCTACGATATTGCTCTCATTTAGTACGATCGATACGATCGATCTTAAACGCTGTG 360  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTyr 140  
 DB 361 CGTTATAGACACAGACACACTGCACTCCCTGAAATTTGGTCAAAATGGTGGCTGTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyPrometIleLeuAlaSerAspSerTyrIleAsnSer 160  
 DB 421 ATACTGGCTTTCTTGGTCAATGGCCCAATGATTTCTGGCTTCGGATTTCTTGGGAACACG 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180  
 DB 481 ACCAACACAGAGAGTGGCAGGCTTGTGTACTGAGTGGTACATCTCGCCATTACA 540

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 541 GCATTTCTTGGAAATTCCTGCTCCCTGCTCTCTTGGTGGTCTATTTCAGTGTACAGATTAC 600  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 601 TGGAGCCTGTGGAGCGTGGAGTCTCAGTAGTGCCCTAGCCACGCTGGATTCTATCGCT 660  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 661 ACCTCTTCAGGGGCACTGGACACTCAGCGCAACTGGGTGGCTTGTAGGACAAAGTCTT 720  
 QY 241 ProGlyLeuLeuGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 DB 721 CTTGATTAAGAAACCCAGCCGCTCCCTTCATTAGAAAGTCCAGAGGAAGAGCAGT 780  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
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 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 841 TTCTCCGATCAGAAAGCCAGTGTCTTACCAGAGAGACGCTGGAGCTTCTCAGAGGC 900  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 901 AGAAAGCTAGCCAGGTGCTAGTCTCTCTCTGAGTGCTTTTGCCATTTGCTGGGCTCG 960  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
 DB 961 TATTGCTGTTTCAAAATTTGCTTTCACATTCAGAGGGGAGGCGCCCAATCGATT 1020  
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 DB 1021 TGGTACAGCATAGCCCTTTTGGCTACAGTGGTTCAATTCACATTATTAATCCCTTCTATAC 1080  
 QY 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 DB 1081 CTTTGTGCCACAGACGTTTCCAGAGGCTTCTGGAAGATACTCTGTGTGCAAGCA 1140  
 QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
 DB 1141 CCAGCACCTTCACAGACCCAGTCAGTATCTTCT 1173  
 AC AAI70981;  
 DT 18-MAR-2002 (first entry)  
 DE Mouse histamine H4 receptor cDNA.  
 KW Histamine H4 receptor; mouse; antiasthmatic; antiallergenic;  
 KW antiinflammatory; cardiant; circulatory; antidiabetic; laxative;  
 KW diagnosis; gene therapy; ss.  
 OS Mus musculus.  
 XX WO200192485-A1.  
 PN 06-DEC-2001.  
 PD 22-FEB-2001; 2001WO-US005914.  
 PF 31-MAY-2000; 2000US-0208260P.  
 PR (ORTH ) ORTHO-MCNEIL PHARM INC.  
 PA Lovenberg T, Liu C;  
 XX WPI; 2002-114339/15.  
 DR

DR P-PSDB; AAM50565.

XX New mammalian histamine H4 receptor proteins and polynucleotides encoding  
 PT the proteins, useful in gene therapy for treating diseases where it is  
 PT beneficial to elevate mammalian histamine H4 receptor activity.

XX Claim 4; Fig 5A; 92pp; English.

XX The present sequence is that of a cDNA clone encoding a murine histamine  
 CC receptor of the H4 subtype. The cDNA was isolated from a mouse spleen  
 CC cDNA library. It shows 72.8% homology to the human H4 receptor coding  
 CC region. The invention provides mammalian (human, mouse, rat and guinea  
 CC pig) histamine H4 receptor nucleic acid molecules (see AAI70980-83) and  
 CC polypeptides (see AAM50564-67). The nucleic acids have been expressed in  
 CC recombinant host cells that produce active recombinant protein. The  
 CC pharmacology of known histamine ligands is demonstrated. Mammalian  
 CC histamine H4 receptor may be used in gene therapy for the treatment of  
 CC diseases where it is beneficial to elevate mammalian histamine H4  
 CC receptor activity. Recombinant protein is useful for identifying  
 CC modulators of the mammalian histamine H4 receptor. Such modulators may be  
 CC useful for diagnosing, treating or preventing asthma, allergy,  
 CC inflammation, cardiovascular and cerebrovascular disorders, non-insulin  
 CC dependent diabetes mellitus, hyperglycemia, constipation, arrhythmia,  
 CC disorders of the neuroendocrine system, stress and spasticity

XX Sequence 1176 BP; 263 A; 281 C; 269 G; 363 T; 0 U; 0 Other;

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 Best Local Similarity: 84.91% Mismatches: 42  
 Query Match: 85.18% Indels: 0  
 DB: Gaps: 6

US-10-626-126-9 (1-391) x AAI70981 (1-1176)

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 DB 1 ATGTGGAGTCTAACAGTACTGTCATCTTCCACAGCTGCTCAGGTCCCTTGGCATTT 60  
 QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 DB 61 TTAATGTCTTCATTGGCTTTGTATTAAGTGTAGGCAATGCTGTGTCATCTTAGGCTTT 120  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
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 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
 DB 181 GACTTCTCTGTGGTGTGATTTCCATTCCTCTGTACATCCCTCAGCGTGTGTTAACTGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 AATTTTGGAGTGGAACTGTCATGTTTGGCTCATTAAGTACATATCTTTTGTGACCGCA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTCTACAAATATTGCTCTCATTAGCTACGATCGATCAGTCAAGTTTCAATGCTGTG 360  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTrp 140  
 DB 361 TCTTATAGGCTCAACACACTGGCATCATGAGATTGTTCTCAAAATGGTGGCTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
 DB 421 ATACTGGCTTTCTTGGTAAATGGCCCGCATGATTTCTGGCTTTCAGATTTCTTGGAAAGACAG 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180  
 DB 481 ACGAACACAAAGGACTGTGAGCTTGGCTTTGTTTACAGAGTGGTACATCTCCACCAATTACA 540

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 541 ATGCTCTTTGGAAATTCCTGCTTCTGTCATCTCTGCTTATTTCAATGTACAGATTTC 600  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 601 TGGAGCTGTGGAAGCTAGGGCTCTCAGTAGTGCCCTAGCCATGCTGGAATTTCTCACT 660  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 661 ACTCTTTCAGTGTCTTCAGGACACTTACACAGAGCTGGGTGGCTTCAGGACAAGTAAT 720  
 QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 DB 721 CTGGGATTCAGGAATCAGCTGCATCTCTGCTACTCAGAAAGTCTCTCGAAGAAAGACAGC 780  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
 DB 781 ATCTGTGTCTTCTTAAAGGACTCAGTACAGCAGTATCTGCTTCAAGTGGGTTC 840  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 841 TTCTGGCGATCGAAAGTCCAGCGCTTCGCCAAAGGGAGTACGACAGCTTCTCAGAGGC 900  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 901 AGGAGCTAGCCAGGTCACTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGTCCA 960  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
 DB 961 TACTGTCTGTTCACAAATGTGCTTTCACTTACCCAGAACGGAACGCCCAATCGGTG 1020  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1021 TGGTACAGCATTCCTTCTGGTGCATGTTGTTCAATTCGTTGTTTAAATCCCTTTCTGTAC 1080  
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 DB 1081 CCTTTGTGTACAGCGCTTTCAGAAAGGCTTTCTGGAAGATATCTTTGTGTGACAAAGCAA 1140  
 QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
 DB 1141 CCAGCCTGTCTACAGAACCAAGTCAATCTTCT 1173  
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 ID ADO30257  
 XX ADO30257 standard; cDNA; 1538 BP.  
 AC ADO30257;  
 DT 29-JUL-2004 (first entry)  
 XX Mouse GPCR HRH4 polynucleotide, SEQ ID NO:1360.  
 DE G protein-coupled receptor; GPCR; drug screening; diagnosis;  
 XX transgenic mouse; neurological disorder; adrenal gland disorder;  
 KW colon disorder; intestinal disorder; cardiovascular disorder;  
 KW muscular disorder; blood disorder; immune disorder; bone disorder;  
 KW joint disorder; metabolic disorder; nutritive disorder; cancer;  
 KW kidney disorder; liver disorder; lung disorder; breast disorder;  
 KW ovary disorder; uterus disorder; prostate disorder; testis disorder;  
 KW skin disorder; stomach disorder; pancreas disorder; spleen disorder;  
 KW thymus disorder; thyroid disorder; antiparkinsonian; antimanic;  
 KW cytotatic; antiinflammatory; vasotropic; antianginal; antirhythmic;  
 KW CNS; central nervous system; respiratory; antidiarrhoeic; antidiabetic;  
 KW virucide; hepatotropic; antibacterial; antianemic; antiseborrhoeic;  
 KW dermatological; antitumor; antithyroid; antiallergic; anorectic;  
 KW immunosuppressive; nephrotropic; gene therapy; GPCR modulator; mouse;  
 KW murine; gene; ss.  
 XX Mus musculus.  
 OS  
 XX WO2004040000-A2.  
 PN

XX 13-MAY-2004.  
 PD 09-SEP-2003; 2003WO-US028226.  
 XX 09-SEP-2002; 2002US-0409303P.  
 XX 09-APR-2003; 2003US-0461329P.  
 XX (PRIM-) PRIMAL INC.  
 PA  
 XX Gaitanaris GA, Bergmann JE, Gragerov A, Hohmann J, Li F;  
 PI Madisen L, McIlwain KL, Pavlova MN, Vassiliadis D, Zeng H;  
 XX WPI: 2004-390329/36.  
 DR P-PSDB; ADO29497.  
 XX  
 PT Novel mammalian G protein coupled receptors, useful for identifying  
 PT compounds that modulates diagnosing and treating disease condition  
 PT associated with GPCR dysfunction e.g. autoimmune diseases, angina  
 PT pectoris, Parkinson's disease.  
 XX  
 PS Claim 151; SEQ ID NO 1360; 542pp; English.  
 XX  
 CC The invention relates to human and mouse G protein-coupled receptors  
 CC (GPCRs) and nucleic acids encoding them. The invention also relates to  
 CC sequences at least 90% identical to the GPCR proteins and nucleic acids  
 CC of the invention; methods of treating, preventing or diagnosing diseases  
 CC associated with GPCRs of the invention; methods of screening for  
 CC compounds useful in the treatment of GPCR-related diseases; a transgenic  
 CC mouse comprising a GPCR gene of the invention; a mouse comprising a  
 CC mutation in a GPCR transgene or in an endogenous GPCR gene; cells derived  
 CC from the transgenic mice; kits comprising several mice, each of which has  
 CC a mutation in a different GPCR gene of the invention; and kits comprising  
 CC probes which hybridize to GPCR polynucleotides of the invention. The  
 CC invention further discloses variants of the GPCR polypeptides and vectors  
 CC comprising a GPCR nucleic acid. The GPCR nucleic acids and proteins may  
 CC be used in the diagnosis, treatment or prevention of a wide variety of  
 CC diseases including neurological disorders (e.g., Alzheimer's disease,  
 CC depression, diabetic neuropathy, Parkinson's disease or schizophrenia);  
 CC disorders of the adrenal gland; disorders of the colon or intestine  
 CC (e.g., Crohn's disease, diarrhoea, food poisoning or irritable bowel  
 CC syndrome); cardiovascular disorders (e.g., angina, cardiac arrhythmia or  
 CC myocardial infarction); muscular disorders; blood disorders (e.g.,  
 CC anaemia or leukaemia); immune disorders (e.g., autoimmune disorders or  
 CC AIDS); bone and joint disorders (e.g., osteoarthritis, rheumatoid  
 CC arthritis, gout or osteoporosis); metabolic or nutritive disorders (e.g.,  
 CC obesity, enzyme deficiency-related diseases or vitamin deficiency-related  
 CC diseases); and disorders of the kidney, liver, lung, breast, ovary,  
 CC uterus, prostate, testis, skin, stomach, pancreas, spleen, thymus and  
 CC thyroid (e.g., cancers). The present sequence represents a GPCR-encoding  
 CC nucleic acid of the invention. Note: The full sequence data for this  
 CC patent did not form part of the printed specification; those sequences  
 CC not shown were obtained in electronic format directly from WIPO at  
 CC ftp.wipo.int/pub/published\_pct\_sequences.  
 XX  
 SQ Sequence 1538 BP; 357 A; 362 C; 340 G; 479 T; 0 U; 0 Other;  
 XX

Alignment Scores:  
 Pred. No.: 1,13e-150 Length: 1538  
 Score: 1742.00 Matches: 332  
 Percent Similarity: 89.26% Conservative: 17  
 Best Local Similarity: 84.91% Mismatches: 42  
 Query Match: 85.18% Indels: 0  
 DB: 12 Gaps: 0

US-10-626-126-9 (1-391) x ADO30257 (1-1538)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 DB 61 ATGTCGGAGCTAAACAGTACTGGCATCTTGGCACACAGCTGCTCAGTCCCTTGGCATTT 120  
 QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 DB 1141 CTTTGTGTGTACAGGGCTTCCAGAGGCTTCTCGAAGATACTTTGTGTGACAAAGCAA 1200  
 QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
 DB 1201 CCAGCGCTGTCAAGAACCAAGTCAGTATCTTCT 1233

DB 121 TTAATGCTCTCATTTGCTTGTATATGTTAGCAATGCTGTGGTCATCTTAGCCTTT 180  
 QY 41 VallalaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 181 GTGGTGGACAGAAACCTTAGACATCGAAGTAATATATTTTCTTAATTTGGCTATTCT 240  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
 DB 241 GACTTCCTCGGGGTTTGAATTCCTCTGTACATCCCTCAGCTGTTGTTTAACTGG 300  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 301 AATTTTGGAGTGAATCTGCATGTTTGGCTCATTACTGACTATCTTTTGTGCACCGCA 360  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 361 TCTGTCTACAATATATTGCTCTCATTTAGCTACGATCCAGTCTAGTTTCAAATCTGTG 420  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140  
 DB 421 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTGCTCAATGGTGGCTGTTGG 480  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
 DB 481 ATACTGGCTTTCTTGGTAAATGGCCCGATGATTTCTGGCTTCAGATTCTTTGGGAAGACAG 540  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180  
 DB 541 ACGAACACAAAGGACTGTGAGCTGGCTTGTGTACAGAGTGGTACATCTCCACCATTACA 600  
 QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 601 ATGCTTTTGGAAATTCCTGCTCTCTGTATCTCTGTGGCTATTTCATGTACAGATTAC 660  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 661 TGGAGCCTGTGAAGCGTAGGCTCTCAGTAGTGGCTAGCCCTAGCCATGCTGGATTCTCCACT 720  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 721 ACCTCTCCAGTGCTTTCAGGACACTTACACAGAGCTGGGTGGTTCGAGGACAAAGTAAT 780  
 QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 DB 781 CTTGATTTGAAGGATACAGTGCATCTGCTACTCAGAAAGTCTCGAAGAAAGAGCAGC 840  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
 DB 841 ATCTCTGGTGTCTTAAGGACTCACATGAACAGCAGTATCATCTTCAAGTGGGTTC 900  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 901 TTCTGGCATCGAAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC 960  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 961 AGAAGCTAGCCAGGTCACTGGCCATCTTTCAGCGCTTTTGGCATTTTGTGGGCTCA 1020  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
 DB 1021 TACTGTCTGTTTCACAATTTGCTCTTCACTTACCACAGAACGCAACGCCCAATTCGGTG 1080  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1081 TGGTACAGCATTTGCTTGGCTGCAATGGTTCATTTGTTTAAATCCCTTTCTGTAC 1140  
 QY 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 DB 1141 CTTTGTGTACAGGGCTTCCAGAGGCTTCTCGAAGATACTTTGTGTGACAAAGCAA 1200  
 QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391  
 DB 1201 CCAGCGCTGTCAAGAACCAAGTCAGTATCTTCT 1233



## RESULT 4

AAD55126

ID AAD55126 standard; DNA; 1170 BP.

XX

AC

AAD55126;

XX

DT 07-AUG-2003 (first entry)

XX

DE Human H4 receptor wild-type DNA #2.

XX

KW Human; H4: histamine receptor; inflammatory bowel disease; psoriasis;  
 KW atopic dermatitis; stroke; myocardial infarction; migraine; allergy;  
 KW chronic obstructive pulmonary disease; COPD; cerebroprotective; therapy;  
 KW rheumatoid arthritis; multiple sclerosis; inflammation; neuroprotective;  
 KW asthma; receptor; gene; ds.

XX

OS Homo sapiens.

XX

FH Key Location/Qualifiers

FT CDS

1. 1170

/\*tag= a

/product= "Human H4 protein"

/note= "CDS does not include stop codon"

FT

/partial

XX

PN W02003020907-A2.

XX

PD 13-MAR-2003.

XX

PF 30-AUG-2002; 2002WO-US027891.

XX

PR 31-AUG-2001; 2001US-0316762P.

PR

13-NOV-2001; 2001US-0332697P.

XX

PA (MERI ) MERCK &amp; CO INC. -

XX

PI Gallagher MJ, Yates SL;

XX

DR WPI; 2003-290186/28.

XX

DR P-PSDB; AAE36417.

XX

Novel splice variants of human H4 histamine receptor, H4b and H4c, useful  
 for identifying agonists or antagonists of the receptor which are useful  
 for treating multiple sclerosis, asthma, allergy, psoriasis and stroke.

XX

PS Disclosure; Page 56-58; 31pp; English.

XX

CC The invention relates to splice variants of human H4 histamine receptor,  
 CC H4b and H4c. The invention is useful for identifying an agonist,  
 CC antagonist or inverse agonist of a mammalian histamine receptor. The  
 CC agonist, antagonist or inverse agonist of H4b and H4c is useful for  
 CC treating inflammation, asthma, allergy, atopic dermatitis, stroke,  
 CC myocardial infarction, migraine, chronic obstructive pulmonary disease  
 CC (COPD), rheumatoid arthritis, multiple sclerosis, inflammatory bowel  
 CC disease, or psoriasis. The present sequence is human H4 receptor DNA

XX

SQ Sequence 1170 BP; 292 A; 245 C; 231 G; 402 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.:	1.37e-119	Length:	1170
Score:	1403.50	Matches:	271
Percent Similarity:	79.34%	Conservative:	40
Best Local Similarity:	69.13%	Mismatches:	78
Query Match:	68.63%	Indels:	3
DB:	9	Gaps:	2

US-10-626-126-9 (1-391) x AAD55126 (1-1170)

QY

1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

Db

1 ATGCCGATACTAATACCAATCAATTATCTAAGCACTCGTGTTAGCAATT 60

XX

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 Db 61 TTTATGTCCTTAGTCTTTTGTCTAATAATGCTAGGAAATGCTTTGGTCACTTTTAGCTTTT 120  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 Db 121 GTGGTGACAAACCTTAGACATCGAAGTAGTATTTTTTTTCTTAACCTGGCCATCTCT 180  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
 Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeuLeuCysThrAla 100  
 Db 241 GATTTTGGAAAGGAAATCTGTGTAATTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 Db 301 TCTGTATATAACATTTGCTCTCATCAGCTATGATCGATACCTGTGCTCTCAATATGCTGTG 360  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTyr 140  
 Db 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrLysAsnSer 160  
 Db 421 GTGCTGGCCCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTTCAGAGCTCTTGAAGAGTAA 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180  
 Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTTGGCATCACA 534  
 QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 Db 535 TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCCTTATTTCAACATGAATATTAT 594  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 Db 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCAAGCCATCTCTGGACTGACTGCT 654  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240  
 Db 655 GTCTCTTCAACATCTGTGGACACTCATTCAGAGGTAGAGTATCTTCAAGGAGATCTCTT 714  
 QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 Db 715 TCTGCATCGACAGAGTCTCTGCATCTTTCATTTCAGAGAGACAGAGAGAGTAGT 774  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
 Db 775 CTCATGTTTCTTCAAGAACCAAGATGAATAGCAATACAAATTCCTTCCAAAATGGGTTC 834  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 Db 835 TTCTCCCAATCAGATTCGTAGCTCTTCCAAAGGGAACATGTTGAACCTGCTTAGAGCC 894  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 Db 895 AGAGATTAGCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTCTGGCTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgGlyGluArgProLysSerIle 340  
 Db 955 TATTCTCTGTTCACAAATGTGCTTTTCATTTTATTCCTCAGCAACAGGCTCTAAATCAGTT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 Db 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCATTTCTTGTCTCAATCTCTTTTGTAT 1074  
 QY 361 ProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 Db 1075 CCATTGTGTACAAAGCGCTTCAAAAGGCTTCTTGAATAATATTTGTATAAAAAGCAA 1134  
 QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391

DB 1135 CCTTACCATCACACACAGTCGGTCAGTATCTTCT 1170

## RESULT 5

ID AAA46023 standard; cDNA; 1173 BP.

XX AC AAA46023;

DT 22-AUG-2000 (first entry)

XX DE Human G protein coupled receptor HRUP7 encoding cDNA SEQ ID NO:13.

XX KW Human; G protein coupled receptor; GPCR; transmembrane receptor; identification; agonist; screening; therapeutic; pharmaceutical; mutant; ss.

XX OS Homo sapiens.

XX PN WO200022131-A2.

XX PD 20-APR-2000.

XX PF 13-OCT-1999; 99WO-US024065.

PR 13-OCT-1998; 98US-00170496.

PR 12-NOV-1998; 98US-0108029P.

PR 20-NOV-1998; 98US-0109213P.

PR 27-NOV-1998; 98US-0110060P.

PR 16-FEB-1999; 99US-0120416P.

PR 26-FEB-1999; 99US-0121852P.

PR 12-MAR-1999; 99US-0123944P.

PR 12-MAR-1999; 99US-0123945P.

PR 12-MAR-1999; 99US-0123946P.

PR 12-MAR-1999; 99US-0123948P.

PR 12-MAR-1999; 99US-0123949P.

PR 12-MAR-1999; 99US-0123951P.

PR 28-MAY-1999; 99US-0136436P.

PR 28-MAY-1999; 99US-0136437P.

PR 28-MAY-1999; 99US-0136439P.

PR 28-MAY-1999; 99US-0137127P.

PR 28-MAY-1999; 99US-0137131P.

PR 28-MAY-1999; 99US-0137567P.

PR 29-JUN-1999; 99US-0141448P.

PR 27-AUG-1999; 99US-0151114P.

PR 03-SEP-1999; 99US-0152524P.

PR 29-SEP-1999; 99US-0156555P.

PR 29-SEP-1999; 99US-0156633P.

PR 29-SEP-1999; 99US-0156634P.

PR 29-SEP-1999; 99US-0156653P.

PR 01-OCT-1999; 99US-0157280P.

PR 01-OCT-1999; 99US-0157281P.

PR 01-OCT-1999; 99US-0157282P.

PR 01-OCT-1999; 99US-0157293P.

PR 01-OCT-1999; 99US-0157294P.

PR 12-OCT-1999; 99US-00416760.

XX 12-OCT-1999; 99US-00417044.

PA (AREN-) ARENA PHARM INC.

XX PI Behan DP, Lehmann-Bruinema K, Chalmers DT, Chen R, Dang HT;

PI Gore M, Liaw CW, Lin I, Lowitz K, White C;

PI WPI; 2000-317986/27.

DR P-PSDB; AAB02831.

XX Non-endogenous, human G protein-coupled receptors for screening receptor,

PT inverse or partial agonists useful as therapeutic agents.

XX Example 1; Page 88-89; 187pp; English.

XX The present invention describes transmembrane receptors, preferably human

CC G protein coupled receptors (GPCR), for which the endogenous ligand is

CC unknown (orphan GPCR receptors). More specifically the present invention  
 CC relates to non-endogenous, constitutively activated versions of a human  
 CC GPCR. These non-endogenous human GPCRs can be useful for the direct  
 CC identification of candidate compounds as receptors agonists, inverse  
 CC agonists or partial agonists for use as pharmaceutical agents. AAA46017  
 CC to AAA46126 and AAB02825 to AAB02859 represent sequences used in the  
 CC exemplification of the present invention

XX  
 SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

## Alignment Scores:

Pred. No.: 1.37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 3 Gaps: 2

US-10-626-126-9 (1-391) x AAA46023 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

DB 1 ATGCCAGATACATAATAGCACAAATCAATTATACATAAGCACTCGTGTACTTTAGCATTT 60

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40

DB 61 TTTATGCTCTTAGTAGCTTTTGTATATATGCTAGGAATGCTTTGGTCAATTTTAGCTTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60

DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTGGCCATCTCT 180

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80

DB 181 GACTTCTTTGTGGGTGTGATCTCCATCTCTTTGTATATCCCTCACACGCTGTTCGAATGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100

DB 241 GATTTTGGAAAGGAATCTGTGTATTTTGGTCACTACTGACTATCTGTATGTACAGCA 300

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120

DB 301 TCTGTATATAACATGTCTCATCAGCTATGATCATGATCATGATCATGATCATGATCATG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTyr 140

DB 361 TCTTATAGAATCAACATCACTGGGTCTTGAAGATTGTACTCTGTGTGCGCCGTTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160

DB 421 GTGCTGGCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGGATGNA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180

DB 481 GGTAGT-----GAATGTGAACCTGGAATTTTTCGAATGGTACATCTCTGCCATCACA 534

QY 181 AlaPheLeuGluPheLeuLeuProValSerIleValValTyrPheSerValGlnIleTyr 200

DB 535 TCATTCTTGAATTCGTATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTyrPheArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220

DB 595 TGGAGCTGTGGAAGCGGTGATCATCTCAGTAGTGGCAAGCCATCTCTGGACTGCTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240

DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTTACAGAGGTAGATATCTTCAAGGAGATCTCT 714

QY 241 ProGlyLeuLeuGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleSerSer 260

DB 715 TCTGCATGCACAGAAGTCTCTGCATCTCTTTCATTCAGAGAGACAGAGGAGAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer 280

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Db 775 TCATGTTTCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGTCC 834
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAACTGCTTAGAGCC 894
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTGGCTGCCA 954
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAATGTCTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGATTGCAATTTGGCTTCAGTGGTTCATTTCTTGTCAATCCTCTTTGTAT 1074
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAAAATATTTTGTATAAAAGCAA 1134
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTTACCATCAACACAGTCGGTCAGTATCTTCT 1170
RESULT 6
AAD01124
ID AAD01124 standard; cDNA; 1173 BP.
XX AC AAD01124;
XX DT 02-NOV-2000 (first entry)
XX DE Human orphan G protein-coupled receptor hRUP7 cDNA.
XX KW Human; orphan G protein-coupled receptor; GPCR; hRUP7; drug screening;
XX KW transmembrane receptor; signal cascade; ss.
XX OS Homo sapiens.
XX FH Key
XX FT CDS
XX FT 1..1173
XX FT /*tag= a
XX FT /product= "hRUP7"
XX FT /note= "Human orphan G protein-coupled receptor"
XX PN WO200031258-A2.
XX PD 02-JUN-2000.
XX PF 13-OCT-1999; 99WO-US023687.
XX PR 20-NOV-1998; 98US-0109213P.
XX PR 16-FEB-1999; 99US-0120416P.
XX PR 26-FEB-1999; 99US-0121852P.
XX PR 12-MAR-1999; 99US-0123946P.
XX PR 12-MAR-1999; 99US-0123949P.
XX PR 28-MAY-1999; 99US-0136436P.
XX PR 28-MAY-1999; 99US-0136437P.
XX PR 28-MAY-1999; 99US-0136439P.
XX PR 28-MAY-1999; 99US-0136567P.
XX PR 28-MAY-1999; 99US-0137127P.
XX PR 28-MAY-1999; 99US-0137131P.
XX PR 29-JUN-1999; 99US-0141448P.
XX PR 29-SEP-1999; 99US-0156535P.
XX PR 29-SEP-1999; 99US-0156536P.
XX PR 29-SEP-1999; 99US-0156634P.
XX PR 01-OCT-1999; 99US-0156653P.
XX PR 01-OCT-1999; 99US-0157280P.
XX PR 01-OCT-1999; 99US-0157281P.
XX PR 01-OCT-1999; 99US-0157282P.
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PR 01-OCT-1999; 99US-0157293P.
PR 01-OCT-1999; 99US-0157294P.
PR 12-OCT-1999; 99US-00416760.
XX 12-OCT-1999; 99US-00417044.
PA (AREN-) ARENA PHARM INC.
XX PI Chen R, Dang HT, Liaw CW, Lin I;
XX DR WPI; 2000-400068/34.
XX DR P-PSDB; AAY71297.
XX PT Novel human orphan G protein-coupled receptors and the encoding cDNAs for
XX PT use in the identification of G protein-coupled receptor agonists.
XX PS Claim 25; Page 59; 102pp; English.
XX CC The present sequence is a cDNA encoding hRUP7, an endogenous human orphan
XX CC G protein-coupled receptor (GPCR). The full length hRUP7 cDNA was cloned
XX CC by RT-PCR using human peripheral leucocyte cDNA as template. The orphan
XX CC GPCR of the invention, like all GPCRs has seven transmembrane alpha
XX CC helices with an extracellular N-terminus and an intracellular C-terminus.
XX CC However, no endogenous ligands has yet been identified for the proteins
XX CC of the invention. The orphan GPCRs may be used in the identification of
XX CC their endogenous ligands, and to screen potential GPCR agonists and
XX CC antagonists for use as pharmaceutical agents. The proteins may also be
XX CC used in the study of GPCR-mediated signalling cascades, and to elucidate
XX CC their precise role in normal and diseased human conditions. Nucleic acid
XX CC encoding human orphan GPCRs may be used for tissue localisation
XX CC expression analysis to provide information about their function in
XX CC healthy and pathological states
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

Alignment Scores:
Pred. No.: 1.37e-119 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 3 Gaps: 2

US-10-626-126-9 (1-391) x AAD01124 (1-1173)
Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATAGCACAATCAATTTATACATAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGCTCTTAGTAGCTTTTGCTATAATGCTAGGAAATGCTTTGCTCATTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACATGGCCATCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTTGGGGTGTGATCTCCATTCTTTGTACATCCCTCACACGCTGTCGATCG 240
Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTGCTCTCATCAGCTATGATACCTGCTCAGTCTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACACTGGGGCTCTGAAGATTGTTACTCTGATGGCGCGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
```

```
Db 421 GTGCTGGCTCTTAGTGAATGGCCCAATGATTCTAGTTTCAGAGTCTTGGAGATGAA 480
:::|||||
Qy 161 ThrAenThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
:::|||||
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTGGCCATCACA 534
:::|||||
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValTyrPheSerValGluIleTyr 200
:::|||||
Db 535 TCATCTCTTGAATTCGGATGCCAGTCACTTAGTCGCTTATTTCACATCAATATTATTTAT 594
:::|||||
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
:::|||||
Db 595 TGGAGCTGTGGAAGCGTGATCATCTCAGTAGTGGCCAAAGCCATCTCTGGAGTCACTGCT 654
:::|||||
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
:::|||||
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
:::|||||
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
:::|||||
Db 715 TCTGATCGACAGAAGTCTCTGATCTCTTTCATTCAGAGACAGAGGAGAAAGATAGT 774
:::|||||
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
:::|||||
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCAATCAATGCTTCCAAATGGTTTC 834
:::|||||
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
:::|||||
Db 835 TTCTCCCAATCAGATCTCTGTAGCTCTTCCACCAAGGGAACATGTTGMACTGCTTAGAGCC 894
:::|||||
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
:::|||||
Db 895 AGGAGATTAGCAAGTCACTGCGCATCTCTTAGGGTTTGTGCTTGTCTGGGCTCCA 954
:::|||||
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
:::|||||
Db 955 TATTCTCTGTTCCAAATGTCTTTCATTTATTTCTCAGCAACAGGTCCTTAATCAGTT 1014
:::|||||
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheLysSerLeuIleAsnProPheLeuTyr 360
:::|||||
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCATCTCTTGTCAATCTCTTTTGTAT 1074
:::|||||
Qy 361 ProLeuCysHisArgArgCysGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
:::|||||
Db 1075 CCATGTGTCAACGCGTTTCAAAAGGCTTCTTGAATAATTTTGTATAAAAGCAA 1134
:::|||||
Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
:::|||||
Db 1135 CCTCTACCATCAACACAGTCGGTCACTATCTTCT 1170
:::|||||
RESULT 7
ID AAF83203 standard; cDNA; 1173 BP.
AC AAF83203;
XX
XX
XX 09-JUL-2001 (first entry)
XX
XX Human GPCR-like polypeptide, PFI-013 encoding cDNA.
XX
XX G-protein coupled receptor; GPCR; PFI-013; antiallergic; antiaesthetic;
KW antiinflammatory; vasotropic; antidiabetic; anorectic; cytotstatic; human;
KW osteopathic; neuroprotective; nootropic; dermatological; gynecological;
KW signal transduction; ss.
XX
XX Homo sapiens.
XX
XX Key Location/Qualifiers
XX CDS 1..1173
XX FT /*tag= a
XX FT /product= "PFI-013"
```

```
PN EP1096009-A1.
XX
PD 02-MAY-2001.
XX
XX 24-OCT-2000; 2000EP-00309364.
XX
XX 29-OCT-1999; 99GB-00025641.
XX
XX 20-APR-2000; 2000GB-00009973.
XX
XX (PFI-013) PFIZER LTD.
XX
XX (PFI-013) PFIZER INC.
XX
XX Peter B, O'reilly MA;
XX
XX WPI; 2001-309854/33.
XX
XX P-PSDB; AAB62445.
XX
XX New G-protein coupled receptor-like polypeptide, polynucleotide for
XX screening drug candidates for treating diseases associated with signal
XX transduction e.g. allergic, inflammatory, pulmonary, neoplastic diseases.
XX
XX Claim 1; Page 43; 66pp; English.
XX
XX This cDNA of NCIMB 41073 encodes a human G-protein coupled receptor
XX (GPCR)-like polypeptide, designated PFI-013. The PFI-013 protein can be
XX expressed by standard recombinant methodology. Antibodies and modulators
XX of PFI-013 are useful in the manufacture of a medicament for treating
XX allergic disorder, including extrinsic asthma, immunological disorders,
XX such as intrinsic asthma, vasculitic granulomatous disease, interstitial
XX and other pulmonary disease, including chronic obstructive pulmonary
XX disease (COPD), infectious, inflammatory disease, such as inflammatory
XX bowel disease and neoplastic and myeloproliferative diseases. They are
XX also useful for treating obesity, diabetes, metabolic, neurological
XX diseases, psychotherapeutics, urogenital disease, reproduction and sexual
XX medicine, inflammation, cancer, tissue repair, dermatology, photoaging,
XX skin pigmentation, osteoporosis, cardiovascular, gastrointestinal
XX diseases, allergy and respiratory disease, sensory organ disorders, sleep
XX disorders and hair loss. The PFI-013 protein and nucleic acid are useful
XX in the diagnosis and treatment of the above conditions and also for
XX screening drug candidates for the treatment of diseases associated with
XX signal transduction. The antibodies are also useful for enrichment of
XX eosinophils from mammalian, especially human blood and for detecting the
XX protein in biological samples
XX
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1.37e-119 Length: 1173
XX Score: 1403.50 Matches: 271
XX Percent Similarity: 79.34% Conservative: 40
XX Best Local Similarity: 69.13% Mismatches: 78
XX Query Match: 68.63% Indels: 3
XX DB: 4 Gaps: 2
XX
XX US-10-626-126-9 (1-391) x AAF83203 (1-1173)
XX
XX Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
XX Db 1 ATGCCAGATCACTAATAGCACAACTTATCATCAAGCACTCGGTGTACTTTCATCATTT 60
XX
XX Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
XX Db 1 TTTATGCTTCTAGTAGCTTTTGTCTATAATGCTAGGAATGCTTTGGTCACTTTTACCTTTT 120
XX
XX Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
XX Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180
XX
XX Qy 61 AspPhePheValGlyValIleSerIleProLeuTrpIleProHisThrLeuPheAsnTrp 80
XX Db 181 GACTTCTTTTGGGGTGTGATCTCCATCTCTTTGTACATCCCTCACACCTGTTCGAATGG 240
XX
XX Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
```





XX Example 1; Col 27-28; 19pp; English.

XX This sequence represents the open reading frame for a human histamine  
 CC receptor (HR) designated SP9144. The sequence was isolated by searching  
 CC databases with the sequence of known G-coupled protein receptor (GPCR).  
 CC The gene is used for recombinant production of HR and for preparing  
 CC antibodies (Ab). These Ab are used to purify HR by immunospecificity  
 CC chromatography, in immunosay of histamine receptor, to identify cDNA  
 CC clones that express the receptor, as antagonist to block binding of  
 CC histamine (for treating any histamine-associated disorder) and to  
 CC generate anti-idiotypic antibodies. Agonists and antagonists of the HR  
 CC protein can be used in the treatment of e.g. inflammation, asthma,  
 CC allergy, atopic dermatitis, stroke, myocardial infarction, migraine,  
 CC chronic obstructive pulmonary disease, rheumatoid arthritis, multiple  
 CC sclerosis, inflammatory bowel disease and psoriasis

XX Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;

#### Alignment Scores:

Pred. No.: 1.37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x ABZ80663 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCCAGATTAATAAGCAGCAATCAATTTATCACTAAGCACTCGGTGTACTTTAGCATTT 60  
 QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40  
 DB 61 TTTATGCTTAGTACTTTTCTAATAAGTAAAGAAATGCTTTGCTCATTTAGCTTTT 120  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTATTTCTTAACCTGGCCATCTCT 180  
 QY 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80  
 DB 181 GACTTCTTTGGTGGTGTATCTCCATTCCTTGTATCCCTCACAGCTGTTTCGAATGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 GAATTTGGAAAGGAATCTGTGTATTTGGCTCACTACTGACTATCTGTATGTAGCAGCA 300  
 QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAACATTGCTCATCATGATGATGATGATGATGATGATGATGATGATGATG 360  
 QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuValIleValAlaGlnMetValAlaValTrp 140  
 DB 361 TCTTATAGAACTCAACATACCTGGGGCTTTGAAGATTGTTACTCTGATGGCGCGTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
 DB 421 GTGCTGGCTCTTCTTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGAAGGATGAA 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180  
 DB 481 GGTAAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCATCTCTGTCATCACA 534  
 QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 535 TCATCTTGGAAATTCGATATCCAGTCCCATCTAGTCGCTTATTTCAACATGAAATATTTAT 594  
 QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 595 TGGAGCTGTGGGAAGCGTGATCTCAGTAGGTGGCAAGCCATCTCTGCACTGACTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 655 GTCTCTTCAACATCTGTGGACACTCATTCACAGGTAGTAGTATTCACAGGAGATCTCT 714  
 QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260  
 DB 715 TCTGTCATCGACAGAGTTCCTGTCATCTTCATTTCAGAGACAGACAGAGAGAGTAGT 774  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280  
 DB 775 CTCATGTTTCTCCTCAAGAACCAAGATGAATAGCAATACAAATGCTTCCAAAATGGGTTC 834  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 835 TTCTCCCAATCAGATTCTGTAGCTCTTTCACCAAGGGAAACATGTTGAACCTGCTTAG 894  
 QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 895 AGAGATTAGCCCAAGTCACTGCGCATTCCTTAGGGGTTTTCGCTGTTGCTGGGTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
 DB 955 TATTCTCTCTTCACAATTCCTCTTTCATTTTATTCCTCAGCAACAGGTCTCTAATCAGT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCATTTCTCTTCTTCTCTTCTTCT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380  
 DB 1075 CCATTTGTGTCAAGCGCTTTCNAAGGCTTCTTGGAAAATATTTTGTATAAAAAGCAA 1134  
 QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
 DB 1135 CCTTACCATCACACACAGTCGTCAGTATCTCTCT 1170

RESULT 10  
 ABQ78739  
 ID ABQ78739 standard; DNA; 1173 BP.  
 XX  
 AC ABQ78739;  
 XX  
 DT 05-DEC-2002 (first entry)  
 XX  
 DE Nucleotide sequence of human histamine receptor.  
 XX  
 KW Human; histamine receptor; receptor; inflammation; asthma; allergy;  
 KW atopic dermatitis; stroke; myocardial infection; migraine;  
 KW chronic obstructive pulmonary disease; COPD; rheumatoid arthritis;  
 KW multiple sclerosis; inflammatory bowel disease; psoriasis;  
 KW intracellular second messenger pathway; cellular growth rate;  
 KW hormone secretion; gene; ss.  
 XX  
 OS Homo sapiens.  
 XX  
 XX Key Location/Qualifiers  
 CDS 1..1173  
 FT /\*tag= a  
 FT /product= "histamine receptor"  
 XX  
 PN US2002098539-A1.  
 XX  
 XX 25-JUL-2002.  
 XX  
 XX 19-MAR-2001; 2001US-00812216.  
 XX  
 XX 07-OCT-1999; 99US-00414010.  
 XX  
 XX (BEH/) BEHAN J X.  
 PA (HEDR/) HEDRICK J A.  
 PA (LAZ/) LAZ T M.  
 PA (MONS/) MONSMA P J.  
 PA (MORS/) MORSE K L.







XX 05-MAY-2000; 2000US-0202151P.  
 PR 23-AUG-2000; 2000US-0227567P.  
 PR 13-NOV-2000; 2000US-0247855P.  
 XX  
 XX (AMHP ) AMERICAN HOME PROD CORP.  
 XX  
 PI Jones PG, Blatcher M, Wu S, Pausch MH;  
 XX  
 XX WPI; 2002-049442/06.  
 DR P-PSDB; AAG66023.  
 XX  
 XX New histamine receptor, termed H4 useful for detecting H4 (ant)agonists  
 PT for treating transplanted organ rejection, asthma, allergy, multiple  
 PT sclerosis and rheumatoid arthritis.  
 XX  
 XX Claim 13; Fig 1; 66pp; English.  
 PS  
 CC The invention provides an isolated histamine receptor, H4, which binds  
 CC ligands comprising imidazole attached to amine by an alkyl chain. The H4  
 CC receptor can be expressed by standard recombinant methodology. Cells  
 CC expressing H4 receptor protein at a detectable level can suppress cyclic  
 CC adenosine monophosphate (cAMP) formation when contacted with the H4  
 CC receptor agonist. The H4 receptor and antibodies are used for identifying  
 CC H4 receptor modulators. Modulation of histamine H4 receptors is useful  
 CC for treating transplanted organ rejection, asthma, allergies and  
 CC autoimmune pathologies such as multiple sclerosis, type 1 diabetes,  
 CC rheumatoid arthritis, cognitive and memory defects. The H4 receptor  
 CC protein and nucleic acids are useful targets to identify drugs that are  
 CC effective in treating disorders associated with histamine-regulated  
 CC processes. Identification and isolation of H4 receptor provides for  
 CC development of screening of molecules that interact with H4 receptors.  
 CC Genetic variants of H4 can be used to diagnose an H4 associated disease  
 CC as described above. The H4 receptor polynucleotide is useful to treat or  
 CC prevent a disorder associated with the function of H4 in peripheral blood  
 CC leukocytes. The present sequence represents a cDNA encoding the human  
 CC histamine H4 receptor protein  
 XX  
 SQ Sequence 1173 BP; 296 A; 245 C; 231 G; 401 T; 0 U; 0 Other;

Alignment Scores:  
 Pred. No.: 1.37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 68.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
 DB: 6 Gaps: 2

US-10-626-126-9 (1-391) x AA167750 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20  
 DB 1 ATGCCAGATACATAATAGCACAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60  
 QY 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40  
 DB 61 TTTATGTCCTTGTAGTCTTTGCTATATAGCTAGGAATGCTTTGTCTATTTAGCTTTT 120  
 QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
 DB 121 GTGGTGGACAAACCTTAGACATCGAAGTACTAGTTATTTTCTTAACITGGCCATCTCT 180  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
 DB 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100  
 DB 241 GATTTTGGAAAGAAATCTGTGTAITTTGGCTCACTACTACTACTACTGTATGTATGACAGA 300  
 QY 101 SerValTyrSerIleValLeuIleGertyrAspArgTyrGlnSerValSerAsnAlaVal 120  
 DB 301 TCTGTATATAACATTTGCTCCTCATCGATGATGATGATGATGATGATGATGATGATGATG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140  
 DB 361 AGTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTACTCTGATCGTGGCCCTTTGG 420  
 QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160  
 DB 421 GTGCTGGCTCTTCTAGTGAATGGGCCAATGATTTCTAGTTTCAGAGTCTTGGAGATGAA 480  
 QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpIleLeuAlaIleThr 180  
 DB 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTTGGCATCACA 534  
 QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200  
 DB 535 TCATTTCTTGGAAATTCGTGATCCCATCTATCTAGTCGCTTATTTCAACATGAATATAT 594  
 QY 201 TrpSerLeuTyrIleAspGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
 DB 595 TGGACCTGTGGAGCGGTGATCATCTCAGTAGTGCCAAAGCCATCTCTGGACTGCTGCT 654  
 QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240  
 DB 655 GTCTCTTCCAACTCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGAGATCTCT 714  
 QY 241 ProGlyLeuIleGluProAlaAlaSerLeuHisSerGluSerProArgGlyIleSerSer 260  
 DB 715 TCTGCATCCAGACAGAGTTCTCTGCATCTTTCATTGAGAGACAGAGAGAGAGATAGT 774  
 QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIleValGlySer 280  
 DB 775 CTCATGTTTTCTCAAGAACCAAGATGATAGCAATCAATTTCTCCAAATGGGTTC 834  
 QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300  
 DB 835 TTCTCCCAATCAGATTCGTAGCTCTTCCAAAGGGAACATGTTGAACTGCTCAGAGCC 894  
 QY 301 ArgIleLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320  
 DB 895 AGGATATTAGCCAGTCACTGGCCATCTCTTAGGGGTTTTTGTCTTGTGGGCTCCA 954  
 QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProIleSerIle 340  
 DB 955 TATTTCTGTGTCACAAATTTGCTCTTTTCAATTTATTTCTCAGCAACAGGCTCTTAATCAGTT 1014  
 QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360  
 DB 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCAATCTCTTTTGTAT 1074  
 QY 361 ProLeuCysHisArgArgPheGlnIleValAlaPheTrpIleLeuCysValThrIleGln 380  
 DB 1075 CCATTTGTGTCAACAGCGCTTTCAAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAA 1134  
 QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391  
 DB 1135 CCTCTACCATCAACACAGCTGGTCACTATCTTCT 1170  
 RESULT 13  
 ID ACA93262  
 XX ACA93262 standard; cDNA; 1173 BP.  
 AC ACA93262;  
 XX  
 DT 16-JUL-2003 (first entry)  
 DE Human cDNA encoding GPCR hRUP7.  
 KW Human; ss: gene; orphan G protein-coupled receptor; GPCR; hARE-3; hARE-4;  
 KW hARE-5; hRUP3; hRUP5; hRUP6; hRUP7; hGPCR27; hARE-1; hARE-2; hRUP1; hG2A;  
 KW hCHN3; hCHN4; hCHN6; hCHN8; hCHN9; hCHN10; hRUF4; signalling cascade.  
 OS Homo sapiens.  
 XX

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PN US2003017528-A1.
XX 23-JAN-2003.
XX 06-JUN-2001; 2001US-00875076.
XX 20-NOV-1998; 98US-0109213P.
XX 16-FEB-1999; 99US-0120416P.
XX 26-FEB-1999; 99US-0121852P.
XX 12-MAR-1999; 99US-0123946P.
XX 12-MAR-1999; 99US-0123946P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136436P.
XX 28-MAY-1999; 99US-0136437P.
XX 28-MAY-1999; 99US-0136439P.
XX 28-MAY-1999; 99US-0136567P.
XX 28-MAY-1999; 99US-0137127P.
XX 28-MAY-1999; 99US-0137131P.
XX 29-JUN-1999; 99US-0141448P.
XX 28-SEP-1999; 99US-0156333P.
XX 29-SEP-1999; 99US-0156555P.
XX 29-SEP-1999; 99US-0156634P.
XX 12-OCT-1999; 99US-00417044.
XX (CHEN/) CHEN R.
XX (DANG/) DANG H T.
XX (LIAN/) LIAN C W.
XX (LINI/) LIN I.
XX Chen R, Dang HT, Liaw CW, Lin I;
XX WPI; 2003-428952/40.
XX P-PSDB; ABU92265.
XX Novel endogenous, orphan, human G protein-coupled receptors useful for
XX identification of modulators of the receptor and as research tools for
XX understanding the role of the receptor in human body.
XX Claim 25; Page 22; 54pp; English.
XX The invention relates to a human G protein-coupled receptor (GPCR)
XX appearing as ABU92259-ABU92277 (encoded by cDNAs ACA93256-ACA93274) named
XX HARE-3, HARE-4, HARE-5, HRUP3, HRUP5, HRUP6, HRUP7, hGPCR27, HARE-1, HARE
XX -2, hPPRI, HG2A, hCHN6, hCHN8, hCHN9, hCHN10 and hRUF4.
XX Also included are a plasmid comprising a vector and one of the cDNAs
XX above and a host cell comprising the plasmid. The GPCRs are useful for
XX the direct identification of candidate compounds as inverse agonists,
XX agonists or partial agonists. In vitro and in vivo systems incorporating
XX GPCRs are useful for elucidating and understanding the roles these
XX receptors play in the human condition, both normal and diseased, as well
XX as understanding the role of constitutive activation as it applies to
XX understanding the signalling cascade. The cDNAs are useful for making a
XX probe for dot-blot analysis against tissue mRNA and/or RT-PCR
XX identification of the expression of the receptor in tissue samples. The
XX present sequence is a cDNA encoding a GPCR of the invention
XX SQ Sequence 1173 BP; 294 A; 245 C; 231 G; 403 T; 0 U; 0 Other;
XX
XX Alignment Scores:
XX Pred. No.: 1-37e-119 Length: 1173
XX Score: 1403.50 Matches: 271
XX Percent Similarity: 79.34% Conservative: 40
XX Best Local Similarity: 69.13% Mismatches: 78
XX Query Match: 68.63% Indels: 3
XX DB: 8 Gaps: 2
XX
XX US-10-626-126-9 (1-391) x ACA93262 (1-1173)
XX
XX QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
XX ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : : |||
XX Db 1 ATCCAGATACTAATAGCAACAAATTTATCATCAAGCACTCGTGTACTTTAGCATTT 60
XX ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : : |||
XX QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
XX ||| : : : : ||| : : : : ||| : : : : ||| : : : : ||| : : : : |||

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Db 955 TATTCTCTGTTTCAAAATGCTTTTCATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014  
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 XX  
 AC ABS57063;  
 XX  
 DT 28-JAN-2003 (first entry)  
 XX  
 DE Human cDNA encoding G-protein coupled receptor AXOR35.  
 XX  
 KW Human; ss; gene; G-protein coupled receptor; AXOR35; lymphocyte;  
 KW macrophage; eosinophil; neutrophil; infection; transplant rejection;  
 KW gastrointestinal disorder; gastric ulcer; inflammatory bowel disease;  
 KW Crohn's disease; irritable bowel syndrome; vomiting; inflammation;  
 KW atopic dermatitis; allergy; autoimmune disorder; rheumatoid arthritis;  
 KW psoriasis; urological disease; urinary retention; cardiovascular disease;  
 KW myocardial infarction; hypotension; hypertension; pulmonary disorder;  
 KW chronic obstructive pulmonary disease; cough; renal disease;  
 KW renal ischaemia; arteriosclerosis; atherosclerosis; psychosis;  
 KW neurological disorder; migraine; anorexia; anxiety; schizophrenia;  
 KW dyskinesia; Parkinson's disease; cancer; obesity; stroke; septic shock;  
 KW graft versus host disease; osteoporosis.  
 XX  
 OS Homo sapiens.  
 XX  
 FH Key Location/Qualifiers  
 FT 1. .1173  
 CDS /\*tag= a  
 FT /\*product= "AXOR35"  
 FT  
 XX US2002137054-A1.  
 FN  
 XX 26-SEP-2002.  
 PD  
 XX 20-JUL-2001; 2001US-00910411.  
 PF  
 XX 02-NOV-1999; 99US-00431898.  
 PR 03-FEB-2000; 2000US-00497790.  
 PR 20-OCT-2000; 2000US-00693761.  
 XX (SMIK ) SMITHKLINE BEECHAM CORP.  
 PA (SMIK ) SMITHKLINE BEECHAM PLC.  
 PI Aubart KM, Bergema DJ, Fitzgerald L, Graybill TL, Li X;  
 PI Michalovich D, Morrow DM, Zhu Y;  
 DR WPI; 2003-074982/07.  
 DR P-PSDB; ABG71960.  
 XX  
 PT Novel isolated G-protein coupled receptor polypeptide, AXOR35, useful for  
 PT treating infections, gastrointestinal disorders, autoimmune disorders,  
 PT urological diseases, cardiovascular diseases and cancer.  
 XX  
 PS Claim 2; Page 21-22; 24pp; English.  
 XX  
 CC The invention relates to an isolated G-protein coupled receptor  
 CC polypeptide, AXOR35, (and its homologues and variants) and its encoding  
 CC polynucleotide (and its homologues, variants, complements and RNA  
 CC equivalents). Also included are an anti-AXOR35 antibody, an AXOR35

CC expression vector, producing a recombinant host cell by introducing the  
 CC vector into a cell such that the host cell produces AXOR35, a membrane of  
 CC the host cell expressing AXOR35, identifying/screening for agonists or  
 CC antagonists of AXOR35 and inhibiting or promoting the function of  
 CC lymphocytes, macrophages, eosinophils, or neutrophils in diseased tissue,  
 CC by administering to the patient AXOR35 agonists or antagonists. The  
 CC agonist or antagonist identified is useful for treating a disease such as  
 CC asthma, or for inhibiting or promoting the function of lymphocytes,  
 CC macrophages, eosinophils, or neutrophils in diseased tissue such as an  
 CC asthmatic lung. AXOR35 or polynucleotide is useful in diagnostic assays,  
 CC for identifying compounds that are agonists or antagonists of AXOR35, as  
 CC vaccines, or for treating infections (bacterial, fungal, protozoan or  
 CC viral infections), transplant rejection, gastrointestinal disorders (such  
 CC as gastric ulcer), inflammatory bowel diseases (such as Crohn's disease),  
 CC irritable bowel syndrome, vomiting, inflammation (such as atopic  
 CC dermatitis), allergy, autoimmune disorders (such as rheumatoid arthritis,  
 CC psoriasis), urological diseases (such as urinary retention),  
 CC cardiovascular diseases (such as myocardial infarction), hypotension,  
 CC hypertension, pulmonary disorders (such as chronic obstructive pulmonary  
 CC disease), cough, renal diseases (such as renal ischaemia),  
 CC arteriosclerosis, atherosclerosis, psychotic and neurological disorders  
 CC (such as migraine, anorexia, anxiety, schizophrenia), dyskinesias (such  
 CC as Parkinson's disease), cancer, obesity, stroke, septic shock, graft  
 CC versus host disease and osteoporosis. The present sequence is the cDNA  
 CC encoding AXOR35  
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 Pred. No.: 1,37e-119 Length: 1173  
 Score: 1403.50 Matches: 271  
 Percent Similarity: 79.34% Conservative: 40  
 Best Local Similarity: 69.13% Mismatches: 78  
 Query Match: 68.63% Indels: 3  
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 Db 61 TTTATGTCTTCTAGTCTTTTGTATTAATGCTAGGAAATGCTTTGTGTCATTTTGTGCTTT 120  
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 Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTTTCTTAACTTGGCCATCTCT 180  
 QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
 Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTATATCCCTCACACGCTGTTTCAATGG 240  
 QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuLeuCysThrAla 100  
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 Db 421 GTGCTGGCCTTCTTAGTGAATGGCCAAATGATTTCTAGTTTACAGATCTTGGAGAGATGAA 480  
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GenCore version 5.1.6  
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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 14:55:30 ; Search time 702 Seconds  
(without alignments)  
3610.526 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

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Searched: 7297361 seqs, 3241162794 residues

Total number of hits satisfying chosen parameters: 14594722

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

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-TRANS=human40.cdi -LIST=45 -DOCALIGN=200 -THR SCORE=pct -THR MAX=100  
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Pred. No. is the number of results predicted by chance to have a

score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

SUMMARIES

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2	2034	99.5	1176	21	US-10-626-126-6 Sequence 6, Appli
3	2034	99.5	1176	21	US-10-626-398-6 Sequence 6, Appli
4	1742	85.2	1176	20	US-10-626-445-5 Sequence 5, Appli
5	1742	85.2	1176	21	US-10-626-126-5 Sequence 5, Appli
6	1742	85.2	1176	21	US-10-626-398-5 Sequence 5, Appli
7	1403.5	68.6	1173	9	US-09-812-216-1 Sequence 1, Appli
8	1403.5	68.6	1173	9	US-09-910-411-1 Sequence 1, Appli
9	1403.5	68.6	1173	10	US-09-875-076-13 Sequence 13, Appl
10	1403.5	68.6	1173	10	US-09-876-252-13 Sequence 13, Appl
11	1403.5	68.6	1173	13	US-10-052-193-1 Sequence 1, Appli
12	1403.5	68.6	1173	15	US-10-272-983-13 Sequence 13, Appl
13	1403.5	68.6	1173	15	US-10-354-769-1 Sequence 13, Appl
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18	1403.5	68.6	1173	19	US-10-782-596-13 Sequence 13, Appl
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22	1403.5	68.6	1173	21	US-10-626-126-1 Sequence 1, Appli
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27	1403.5	68.6	3689	15	US-10-225-567A-628 Sequence 628, App
28	1403.5	68.6	3689	21	US-10-684-206-19 Sequence 19, Appl
29	1398.5	68.4	1265	15	US-10-290-078-26 Sequence 25, Appl
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32	1237.5	60.5	1170	21	US-10-626-126-7 Sequence 7, Appli
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38	693	33.9	1335	19	US-10-727-021-6 Sequence 6, Appli
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44	693	33.9	2689	15	US-10-282-958-1 Sequence 1, Appli
45	693	33.9	2699	15	US-10-225-567A-548 Sequence 548, App

ALIGNMENTS

RESULT 1

US-10-626-445-6  
; Sequence 6, Application US/10626445  
; Publication No. US20040248252A1  
; GENERAL INFORMATION:  
; APPLICANT: Lovenberg, Timothy  
; APPLICANT: Liu, Changlu  
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype  
; FILE REFERENCE: PRD-0032  
; CURRENT APPLICATION NUMBER: US/10/626,445  
; PRIOR FILING DATE: 2003-07-23  
; PRIOR APPLICATION NUMBER: 09/790,849  
; PRIOR FILING DATE: 2001-02-22  
; PRIOR APPLICATION NUMBER: 60/208,260  
; PRIOR FILING DATE: 2000-05-31  
; NUMBER OF SEQ ID NOS: 27

! SOFTWARE: PatentIn version 3.2

! SEQ ID NO 6

! LENGTH: 1176

! TYPE: DNA

! ORGANISM: Rattus rattus

US-10-626-445-6

Alignment Scores:

Pred. No.: 4,28e-215 Length: 1176  
Score: 2034.00 Matches: 390  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.46% Indels: 0  
DB: 20 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-6 (1-1176)

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QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGTCCTCTGCTTTTGTCTATAAGATAGGCAATGCTGTGGTCAATTTAGCCTTT 120
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QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTCGTGGGTGTCATCTCCATCTCTGTATACCTCCCTCACAGCTGTTTAACGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100
Db 241 AATTTTGAAGTGAATCTGCAATGTTTGGCTCATTAAGTCTGCTGCTGCTGCTGCTG 300
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QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140
Db 361 CGTTATAGACACAGACACACACACACACACACACACACACACACACACACACACACAC 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIleAsnSer 160
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QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpIleLeuAlaIleThr 180
Db 481 ACCAACACAGAGAGTGGAGCTGCTTTGTTACTGAGTGTATACATCTCCCAATTAACA 540
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RESULT 2

US-10-626-126-6

! Sequence 6, Application US/10626126

! Publication No. US20050074770A1

! GENERAL INFORMATION:

! APPLICANT: Lovenberg, Timothy

! TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype

! FILE REFERENCE: PRD-0033

! CURRENT APPLICATION NUMBER: US/10/626,126

! PRIOR FILING DATE: 2003-07-23

! PRIOR APPLICATION NUMBER: 09/790,849

! PRIOR FILING DATE: 2001-02-22

! PRIOR APPLICATION NUMBER: 60/208,260

! PRIOR FILING DATE: 2000-05-31

! NUMBER OF SEQ ID NOS: 27

! SOFTWARE: PatentIn version 3.2

! SEQ ID NO 6

! LENGTH: 1176

! TYPE: DNA

! ORGANISM: Rattus rattus

US-10-626-126-6

Alignment Scores:

Pred. No.: 4,28e-215 Length: 1176  
Score: 2034.00 Matches: 390  
Percent Similarity: 99.74% Conservative: 0  
Best Local Similarity: 99.74% Mismatches: 1  
Query Match: 99.46% Indels: 0  
DB: 21 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-6 (1-1176)

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Db 1 ATGTCGGAGCTAAACGGCACTGACGCTTGGCCACTGACTGCTCAAGTCCCTTGGCATTT 60
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Db 61 TTAATGTCCTCTGCTTTTGTCTATAAGATAGGCAATGCTGTGGTCAATTTAGCCTTT 120
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QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
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QY 141 IleLeuAlaPheLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 160
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QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180
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DB 721 CCTGGATTAAAGCAACAGCGCATCCCTTCATTCAGAAAGTCCACGAGGAAGACAGT 780
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
DB 781 CTCCTGGTGTCTTAAGGACTCATGAGCGGTAGTATCATCGCCTTCAAAGTGGGTTC 840
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
DB 841 TTCTGCGGATCAGAAAGCCAGCGTCTCACCAGAGAGAGACCGTGGAGCTTCTCAGAGGC 900
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
DB 901 AGGAAGCTAGCACAGTTCGTAGTGTCTCTCCTGAGTGTCTTGGCATTTGCTGGGCTCG 960
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
DB 961 TATTGGCTGTTCACAATTGTTCTTTCAACTTATCGCAGAGAGAGCGGCCCAAAATCGATT 1020
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
DB 1021 TGGTACAGCATAGCCCTTTGGCTACAGTGGTTCATTAATTCATTCCTCTTCTATATAC 1080
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
DB 1081 CCTTTGGCCACAGAGCTTTCCAGAGGCTTTCTGGAAGGATCTCTGTGTGACAAAGCAA 1140
QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391
DB 1141 CCAGCACCTTCACAGACCCAGTCAATCTCTCT 1173
```

## RESULT 3

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US-10-626-398-6
; Sequence 6, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; APPLICANT: Liu, Changlu
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
```

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; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 6
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Rattus rattus
; US-10-626-398-6
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## Alignment Scores:

Pred. No.:	4,28e-215	Length:	1176
Score:	2034.00	Matches:	390
Percent Similarity:	99.74%	Conservative:	0
Best Local Similarity:	99.74%	Mismatches:	1
Query Match:	99.46%	Indels:	0
DB:	21	Gaps:	0

US-10-626-126-9 (1-391) x US-10-626-398-6 (1-1176)

```
QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB 1 ATGTGCGAGCTTAACGCGACTGACGCTTGCCTCACTGCTCAAGTCCCTTTGGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
DB 61 TTAATGTCCTGCTTCTTCTTGTATACGATAGGCAATGCTGTGTGCTCAATTTAGCCTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTAGCAGACAGAAACCTTAGACATCGAAGTAATTAATTTTCTTAATTTGGCTATTTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIlePheProHisThrLeuPheAsnTyr 80
DB 181 GACTTCTCGTGGGTGTCATCTCCATTCCTCTGTACATCCCTCACACGCTGTTTAACTGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 AATTTTGGAAAGTGAATCTGCATGTTTGGCTCATTAAGTACATCTTTTGTGCGACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCGGTCTACAGATTGTTCTCTCATTAAGTACATCGATCGATCGATCGATCGATCGATCG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
DB 361 CGTTATAGACACAGACACAGTGCATCTGAAATTTGCTCAAAATGGTGGCTGTTTGG 420
QY 141 IleLeuAlaPheLeuValLeuValLeuValLeuValLeuValLeuValLeuValLeu 160
DB 421 ATACTGGCTTTCTTGTGTCAATGCGCCCAATGATTCGTGGCTTCGGAATTCCTTGG 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180
DB 481 ACCAACACAGAGAGTGGAGTCTCAGTAGTGCCCTAGCCAGCCGCTGGAATTCATCG 540
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 541 GCATTCCTGGAAATTCCTGCTCCCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCTGCT 600
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerLeuSerLeuSerLeuSerLeuSerLeu 220
DB 601 TGGAGCCTGTGGAAGCGTGGAGTCTCAGTAGTGCCCTAGCCAGCCGCTGGAATTCATCG 660
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB 661 ACCTCTTCAGGGGCACTGGACACTCAGCAGAACTGGGTGGCTTGTAGGACAGTCTT 720
QY 241 ProGlyLeuLysGluProAlaLeuSerLeuHisSerGluSerProArgGlyLysSerSer 260
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Db 721 CCTGGATTAAAGAACACAGCGCATCCCTTCATTAGAAAGTCCAGAGAAAGAGCAGT 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 CTCCTGGGTGCTCCTTAAGGACTCACATGAGCGTAGTATCATCGCCTTCAAAGTGGGTTC 840
Qy 281 PheCysArgSerGlySerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCCTCCGATCAGAAGCCAGTGTCTTACCAGAGAGACAGTGGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTGCTAGCTGCTCCTCCTAGTGTCTTTGGCATTGTGGGCTCG 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TATTGCTGTTTACAAATTGTTCTTCACTTATCGCAGAGGGAGCGGCCCAATCGATT 1020
Qy 341 TrpTyrSerIleAlaPheThrLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATAGCCTTTGGCTACAGTGTTCATTTCAATTCATTATTAATCCCTTTCTATAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheThrLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGCCACAGACGTTTCCAGAAAGGCTTCTCGAAGATACTCTGTGTGACAAAGCAA 1140
Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CCAGCACCTTCACAGACCCAGTCAGTATCTTCT 1173

RESULT 4
US-10-626-445-5
; Sequence 5, Application US/10626445
; Publication NO. US20040248252A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNA Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0032
; CURRENT APPLICATION NUMBER: US/10/626,445
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-445-5

Alignment Scores:
Pred. No.: 1,12e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.26% Conservatives: 17
Best Local Similarity: 84.91% Mismatches: 42
Query Match: 85.18% Indels: 0
DB: 20 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-445-5 (1-1176)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGTCCGAGCTAAACAGTACTGGCATCTTGCACACAGCTGCTCAGGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGCTTCATTGCTTCCCTTTGCTATATGAGGCAATGCTGTGTGCTATCTAGCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 1173
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RESULT 5

US-10-626-126-5

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; Sequence 5, Application US/10626126
; Publication No. US20050074770A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0033
; CURRENT APPLICATION NUMBER: US/10/626,126
; PRIOR FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-126-5

Alignment Scores:
Pred. No.: 1,12e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.26% Conservatives: 17
Best Local Similarity: 84.91% Mismatches: 42
Query Match: 85.18% Indels: 0
DB: 21 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-126-5 (1-1176)
QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThraGlnValProLeuAlaPhe 20
DB 1 ATGTCGGAGTCTAACAGTACTGGCATCTTGCCACCAGCTGCTCAGGTCCTCCCTTTGGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
DB 61 TTAATGCTCTCATTTGCTTGTATTAATGTTAGGCAATGCTGTGGTCTATCTTGGCTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGGACAGAACCTTAGACATCGAAGTAATATTTTCTTAATTTGGCTATTTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB 181 GACTTCTCTGGGTTGATTTCATTCCTCTGTACATCCTCAGCGTTGTTGTTAACTGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrTrpLeuLeuCysThrAla 100
DB 241 AATTTTGGAGTGGAAATCTGCATGTTTGGCTCATTACTGACTATATCTTTTGTGACCGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB 301 TCTGTCTACAAATATTGCTCATTAGCTAGCATCGATACAGTCAGTTCATTAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTrp 140
DB 361 TCTTATAGGCTCAACACACTGGCATCATGAAGATTGTTCTCAATGGTGGCTGTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 ATACTGGCTTTCTTGGTAAATGGCCGATGATTCCTGGCTTCAGATTCTTGGAAAGACAGC 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
DB 481 ACCAACAACAAGACTGTGAGCTGGCTTTGTACAGAGTGGTACATCCTCACCAATTACA 540
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 541 ATGCTCTTGGAAATTCCTGCTTCTGTGTCATCTGTGGCTATTATTCATGTACAGATTAC 600
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
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DB 601 TGGAGCCTCTGGAAGCGTAGGCTCTCAGTAGTGCCCTAGCCANCTGGATTCTCACT 660
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB 661 ACCTCTTCAGTCTTCAGGACACTTACACAGAGCTGGGGTGGCTTGACGAGCAAGTAAT 720
QY 241 ProGlyLeuLysGluProAlaIleSerLeuHisSerGluSerProArgGlyLysSerSer 260
DB 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCTGAAAGAGAGCAGC 780
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
DB 781 ATCTGTGTCTCTTAAGGACTCACATGAACAGCAGTATCACTGCCITCAAAGTGGGTTC 840
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
DB 841 TTCTGGCGATCGAAGTGCAGCGCTTCGCCAAAGGGAGTACGCAGAGCTTCTCAGAGGC 900
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
DB 901 AGGAAGCTAGCCAGGTCAGTGGCCATCTTCTGAGCGCTTTTGCCATTTGCTGGGTCCA 960
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
DB 961 TACTGTCTGTTCACAATGTGCTTTCACTTACCCAGAACGAGACGCCCAATCGGTG 1020
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
DB 1021 TGGTACAGCATTTGCCCTTCTGGCTGCAATGGTTCATTCGTTTGTAAATCCCTTTCTGTAC 1080
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
DB 1081 CCTTTGTGTACAGCGGTTTCCAGAGGCTTTCTGGAAGATACTTTGTGTGACAAAGCAA 1140
QY 381 ProAlaProSerGlnThrGlnSerValSerSer 391
DB 1141 CCAGCGCTGTACAGAAACCCAGTATCTTCT 1173

RESULT 6
US-10-626-398-5
; Sequence 5, Application US/10626398
; Publication No. US20050074841A1
; GENERAL INFORMATION:
; APPLICANT: Lovenberg, Timothy
; TITLE OF INVENTION: DNAs Encoding Mammalian Histamine Receptor Of The H4 Subtype
; FILE REFERENCE: PRD-0034
; CURRENT APPLICATION NUMBER: US/10/626,398
; CURRENT FILING DATE: 2003-07-23
; PRIOR APPLICATION NUMBER: 09/790,849
; PRIOR FILING DATE: 2001-02-22
; PRIOR APPLICATION NUMBER: 60/208,260
; PRIOR FILING DATE: 2000-05-31
; NUMBER OF SEQ ID NOS: 27
; SOFTWARE: Patent in version 3.2
; SEQ ID NO 5
; LENGTH: 1176
; TYPE: DNA
; ORGANISM: Mus musculus
US-10-626-398-5

Alignment Scores:
Pred. No.: 1,12e-182 Length: 1176
Score: 1742.00 Matches: 332
Percent Similarity: 89.26% Conservatives: 17
Best Local Similarity: 84.91% Mismatches: 42
Query Match: 85.18% Indels: 0
DB: 21 Gaps: 0

US-10-626-126-9 (1-391) x US-10-626-398-5 (1-1176)
QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThraGlnValProLeuAlaPhe 20
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Db 1 ATGTCGAGCTCTAACAGTACTGGCATCTTGGCCACAGCTGTCTCAGTCCCTTGGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTAATGTCTTCAATTTGGCTTTGCTATAATGGTAGCAATGCTGTGCTCATCTTAGCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAGAACTTAGACATCGAAGTAATATTTTTTTCTTAATTTGGCTATTTCT 180
Qy 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTCGTGGGTTTGATTTCCATCTCTGTATCATCCCTCACGTGTTGTTAACTGG 240
Qy 81 AnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 AATTTTGGGAAGTGAATCTGCATGTTTGGCTCATTTACTGACTATCTTTTGGCCCGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTCTCAATATTTGCTCTATTAGTACGATCGATACCATGCTGATTTCAATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGGCTCAACACACTGGCATGAAGATTGTTGCTCAAAATGGTGGCTGTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 ATACTGGCTTTCTTGGTAAATGCCCGATGATCTTGGCTTCAGATCTTTGGGAAGACAGC 480
Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpIleLeuAlaIleThr 180
Db 481 ACGAACACAAAGGACTGTGAGCTGGCTGTTGTACAGAGTGTATCATCTCCATTACA 540
Qy 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 541 ATGCTCTTGGAAATCTCTGCTTCTGTCACTCTGTGGCTTATTTCAATGTACAGATTTAC 600
Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 601 TGGAGCCTGTGGAAGCTTAGGGCTCTCAGTAGTGCTCCCTAGCCATGCTGGATTCTCCACT 660
Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 661 ACCTCTTCAGTGCTTCAGACACTTACACAGAGCTGGGTGGCTTGCAGACAGTAAT 720
Qy 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 721 CCTGGATTGAAGGAATCAGCTGCATCTCGTCACTCAGAAAGTCTCGAAGAAAGAGCAGC 780
Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
Db 781 ATCTCTGGTGTCTTAAGGACTCACATGAACAGCAGTATCATCGCTTCAAAAGTGGGTGCC 840
Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 841 TTCCTGGCATCGGAAGTGCAGCGCTTCCCAAAGGAGTAGCAGAGCTTCTCAGAGGC 900
Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 901 AGGAAGCTAGCCAGGTCACCTGGCCATCTCTGAGCGCTTTTGGCATTTGCTGGGCTCCA 960
Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 961 TACTGTCTGTTTCACAATTTGCTTTCACTTACCCAGAACAGCAAGCGCCCAAAATGGGTG 1020
Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1021 TGGTACAGCATTTGGCTTCTGGCTGCAATGTTTCAATTCCTTTGTTAAATCCCTTTCTGTAC 1080
Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1081 CCTTTGTGTACAGGCGTTTCCAGAAGGCTTTCTCGAAGATACTTTGTGTGACAAAGCAA 1140
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Qy 381 ProAlaProSerGlnThrGlnSerValSerSer 391
Db 1141 CACGCGCTGTACAGAACCAAGTCAGTATCTTCT 1173
```

## RESULT 7

US-09-812-216-1

; Sequence 1, Application US/09812216

; Patent No. US20020098539A1

; GENERAL INFORMATION:

; APPLICANT: Behan, Jiang Xu

; APPLICANT: Hedrick, Joseph A.

; APPLICANT: Laz, Thomas M.

; APPLICANT: Monama, Frederick J. Jr.

; APPLICANT: Morse, Kelley L.

; APPLICANT: Umland, Shelby P.

; APPLICANT: Wang, Suke

; TITLE OF INVENTION: Histamine receptor

; FILE REFERENCE: CN01069

; CURRENT APPLICATION NUMBER: US/09/812,216

; CURRENT FILING DATE: 2001-03-19

; PRIOR APPLICATION NUMBER: 09/414,010

; NUMBER OF SEQ ID NOS: 8

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 1

; LENGTH: 1173

; TYPE: DNA

; ORGANISM: Homo sapiens

US-09-812-216-1

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Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 9 Gaps: 2
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US-10-626-126-9 (1-391) x US-09-812-216-1 (1-1173)

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Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCATTAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCTTAGTAGCTTTTGTCTATAATGCTAGGAAATGCTTTGCTCATTTTAGCTTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTTTTTCTTAACCTGGCCATCTCT 180
Qy 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db 181 GACTTCTTTGGTGGTGTGATCTCCATTTCTTTGTATACATCCCTCACAGCTGTTGGAATGG 240
Qy 81 AnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGCAAAATCTGTATTTTGGCTCACTACTGACTATCTGTTATGTACAGCA 300
Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTCTCTCATCAGCATGATCATCTGCTAGTCTCAATATGCTGTG 360
Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
Db 361 TCTTATAGAACTCAACATACATAGGCTTTGAAGATTGTTACTCTGCTGCGCGCTTGG 420
Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGAGTCTTTGGGAAGGATGAA 480
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QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTCGGAATGGTACATCTCTTGCATCACA 534

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTGGAAATTCGTATCCAGTCATCTTAGTCCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCTCAGTAGGTGCGCAAGCCATCTCTGGACTGACTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAGTTCCTGCATCTCTTCATTCAGAGAGACAGAGGAGAAAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280
Db 775 CTCATGTGTTTCTCAAGAACCAAGATGAATAGCAATACAAATTCCTCCAAATGGGTCC 834

QY 281 PheCysArgSerGluSerProValLeuHisGluArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAACCTGCTTAGAGCC 894

QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATTAGCAAGTCACCTGGGCATCTCTTAGGGGTTTTGCTGTCTGCTGGCTCCA 954

QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATCTCTGTTCACAAATGTCCTTCATTTTATCTCCACACACAGCTCTCAATCAGTT 1014

QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAAATTCATTTTGGCTTCAGTGGTTCAATTCCTTTGTCATCTCTTTGTAT 1074

QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTTGTCCAAAGCGCTTCAAAAGCGCTTCTTGAAAATATTTGTATAAAAAGCAA 1134

QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGCTCGGTACGTATCTCT 1170
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## RESULT 8

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US-09-910-411-1
; Sequence 1, Application US/09910411
; Patent No. US20020137054A1
; GENERAL INFORMATION:
; APPLICANT: Bergsma, Derek
; APPLICANT: Fitzgerald, Laura
; APPLICANT: Li, Xiaotong
; APPLICANT: Michalovich, David
; APPLICANT: Zhu, Yuan
; TITLE OF INVENTION: AXOR35, A G-Protein Coupled Receptor
; FILE REFERENCE: GP70655-2C1
; CURRENT APPLICATION NUMBER: US/09/910,411
; CURRENT FILING DATE: 2001-07-20
; PRIOR APPLICATION NUMBER: 09/693,761
; PRIOR FILING DATE: 2000-10-20
; PRIOR APPLICATION NUMBER: 09/497,790
; PRIOR FILING DATE: 2000-02-03
; PRIOR APPLICATION NUMBER: 09/431,898
; PRIOR FILING DATE: 1999-11-02
; NUMBER OF SEQ ID NOS: 2
; SOFTWARE: Fast-Seq for Windows Version 4.0
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
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; ORGANISM: Homo sapien
US-09-910-411-1
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Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservatives: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 9 Gaps: 2
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US-10-626-126-9 (1-391) x US-09-910-411-1 (1-1173)
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QY 21 LeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTGTAGTCTTTTGTCTATAATGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTCGACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCT 180

QY 61 AspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACAGCTGTTTGAATGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrIleLeuCysThrAla 100
Db 241 GATTTTGGAAAGAAATCTGTGTATTTTGGCTCACACTGACTATCTGTTATGTACAGCA 300

QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAACATTTGCTCTCATCAGCATATGATCGATCTGTCAGTCTCAATGTGTG 360

QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGGTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGAGTCTTGGAAAGTAA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGGTACATCTCTTGCATCACA 534

QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
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QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAAGCGTGATCTCAGTAGGTGCGCAAGCCATCTCTGGACTGACTGCT 654

QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCCTGCATCTCTTTCATTCAGAGAGACAGAGGAGAAAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280
Db 775 CTCATGTGTTTCTCAAGAACCAAGATGAATAGCAATACAAATTCCTCCAAATGGGTCC 834

QY 281 PheCysArgSerGluSerProValLeuHisGluArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACCAAGGGAACATGTTGAATCTGCTTAGAGCC 894
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QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340  
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## RESULT 9

US-09-875-076-13  
; Sequence 13, Application US/09875076  
; Publication No. US20030017528A1  
; GENERAL INFORMATION:  
; APPLICANT: Chen, Ruoping  
; APPLICANT: Dang, Huong T.  
; APPLICANT: Liaw, Chen W.  
; APPLICANT: Lin, I-Lin  
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors  
; FILE REFERENCE: AREN0050  
; CURRENT APPLICATION NUMBER: US/09/875,076  
; CURRENT FILING DATE: 2001-06-06  
; PRIOR APPLICATION NUMBER: 09/417,044  
; PRIOR FILING DATE: 1999-10-12  
; PRIOR APPLICATION NUMBER: 60/120,416  
; PRIOR FILING DATE: 1999-02-16  
; PRIOR APPLICATION NUMBER: 60/121,851  
; PRIOR FILING DATE: 1999-02-26  
; PRIOR APPLICATION NUMBER: 60/123,946  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/123,949  
; PRIOR FILING DATE: 1999-03-12  
; PRIOR APPLICATION NUMBER: 60/136,436  
; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-05-28  
; PRIOR APPLICATION NUMBER: 60/137,131  
; PRIOR FILING DATE: 1999-05-28  
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; PRIOR FILING DATE: 1999-06-29  
; PRIOR APPLICATION NUMBER: 60/156,653  
; PRIOR FILING DATE: 1999-09-29  
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; PRIOR FILING DATE: 1999-09-29  
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; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/156,634  
; PRIOR FILING DATE: 1999-09-29  
; PRIOR APPLICATION NUMBER: 60/157,280  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,294  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,281  
; PRIOR FILING DATE: 1999-10-01  
; PRIOR APPLICATION NUMBER: 60/157,293  
; PRIOR FILING DATE: 1999-10-01

; PRIOR APPLICATION NUMBER: 60/157,282  
; PRIOR FILING DATE: 1999-10-01  
; NUMBER OF SEQ ID NOS: 74  
; SOFTWARE: PatentIn Ver. 2.1  
; SEQ ID NO 13  
; LENGTH: 1173  
; TYPE: DNA  
; ORGANISM: Homo sapiens  
; US-09-875-076-13  
Alignment Scores:  
Pred. No.: 4,25e-145 Length: 1173  
Score: 1403.50 Matches: 271  
Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 10 Gaps: 2  
US-10-626-126-9 (1-391) x US-09-875-076-13 (1-1173)  
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Db 1 ATGCCAGATACCTAATAGCACAAATCAATTTATCACTAAGCACCTCGTGTACTTTAGCATTT 60  
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40  
Db 61 TTTATGTCTTAGTAGCTTTTGTATATATGCTAGGAAATGCTTTGTCTCAATTTAGCTTTT 120  
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60  
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGCCATCTCT 180  
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80  
Db 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240  
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QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140  
Db 361 TCTTATAGAACTCAACATACCTGGGGTCTTGAAGATTGTTACTCTGATGTCGCGCTTGG 420  
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160  
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QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpIleLeuAlaIleThr 180  
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTCGGAATGTTGATCATCTTCCATCACA 534  
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QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220  
Db 595 TGGAGCTTGTGGAGCGGTGATCATCTCAGTAGTGTCCAAAGCCATCCTCGACTGCTGCT 654  
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QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280

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Db 895 AGGAGATTAGCAAGTCACTGGCCATTCTCTTAGGGGTTTTGCTGTGTTCTGGGTCCA 954
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RESULT 10
US-09-876-252-13
; Sequence 13, Application US/09876252
; Publication No. US20030018182A1
; GENERAL INFORMATION:
; APPLICANT: Behan, Dominic P.
; APPLICANT: Lehmann-Bruinsma, Karin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Lowitz, Kevin P.
; APPLICANT: Lin, I-Lin
; APPLICANT: Dang, Huong T.
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; TITLE OF INVENTION: Non-Endogenous Constitutively Activated Human G Protein Coupled Re
; FILE REFERENCE: AREN-0054
; CURRENT APPLICATION NUMBER: US/09/876,252
; CURRENT FILING DATE: 2001-06-07
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/152,524
; PRIOR FILING DATE: 1999-09-03
; PRIOR APPLICATION NUMBER: 60/151,114
; PRIOR FILING DATE: 1999-08-27
; PRIOR APPLICATION NUMBER: 60/108,029
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; PRIOR FILING DATE: 1998-11-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
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; PRIOR FILING DATE: 1999-06-29
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/156,555
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,634
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/156,653
; PRIOR FILING DATE: 1999-09-29
; PRIOR APPLICATION NUMBER: 60/157,280
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,294
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,281
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/157,282
; PRIOR FILING DATE: 1999-10-01
; PRIOR APPLICATION NUMBER: 60/156,633
; PRIOR FILING DATE: 1999-09-29
; NUMBER OF SEQ ID NOS: 146
; SOFTWARE: PatentIn version 3.0
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-09-876-252-13

Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 10 Gaps: 2

US-10-626-126-9 (1-391) x US-09-876-252-13 (1-1173)
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Db 1 ATGCCAGATACATAATAGCACAAATCAATTTATCACTAAGCACTCGTGTACTTTAGCATTT 60
Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCTTGTAGTCTTTTGTCTATAATGCTAGGAAATGCTTTGTGTCATTTTGTGCTTT 120
Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGCACAAAACCTTAGACATCGAAGTAGTATATTTTCTTAACCTTGGCACTCTCT 180
Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGTGGGTGTGATCTCAATTCCTTTGTACATCCCTCACAGCTGTTTCAATGG 240
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QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GTGCTGGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGAGTCTTTGGGAAGGATGAA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
DB 481 GGTAGT-----GAATGTGAACCTGGATTCTTTCGGAATGGTACATCCTTGCCATCACA 534

QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 535 TCATTCTTGGAAATTTGTGATCCAGATCATCTCTAGTCGCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB 595 TGGAGCCTGTGGAAGCGTGATCATCTCAGTAGGTGCCAAAGCCATCCTGGACTGCTGCT 654

QY 221 ThrSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB 655 GTCTTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
DB 715 TCTGCATCGACAGAGTCTCTGCATCCTTTCATTTCAGAGAGACAGAGGAGAAGAGTAGT 774

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QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
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QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
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QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
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QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
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QY 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
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## RESULT 11

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US-10-052-193-1
; Sequence 1, Application US/10052193
; Publication No. US20020132755A1
; GENERAL INFORMATION:
; APPLICANT: Pfizer, Inc.
; TITLE OF INVENTION: HISTAMINE RECEPTOR ANTAGONISTS
; FILE REFERENCE: PC10963A
; CURRENT APPLICATION NUMBER: US/10/052,193
; PRIOR FILING DATE: 2002-01-17
; PRIOR APPLICATION NUMBER: 0101223.6
; NUMBER OF SEQ ID NOS: 10
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 1
; LENGTH: 1173
; TYPE: DNA
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; ORGANISM: Homo sapiens
US-10-052-193-1
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## Alignment Scores:

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Score: 4.25e-145 Length: 1173
Pred. No.: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 13 Gaps: 2
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US-10-626-126-9 (1-391) x US-10-052-193-1 (1-1173)

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QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB 1 ATGCCAGATATAATAGCACAAATCAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60

QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
DB 61 TTTATGTCCTTAGTAGCTTTTGTATATAATGCTAGGAATGCTTTGGTCATTTTACGTTT 120

QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTTGCCATCTCT 180

QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB 181 GACTTCTTTGTGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240

QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB 241 GATTTTGGAAAGGAATCTGTGTATTTTGGTCACTACTGACTATCTGTTATGTACAGCA 300

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QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTyr 140
DB 361 TCTTATAGAACTCAACATACTGGGCTCTGAAGATTGTACTCTGATGGTGCCGTTTGG 420

QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
DB 421 GTGCTGGGCTTCTTAGTGAATGGGCAATGATTTCTAGTTTTCAGAGTCTTTGGGAAGGATGAA 480

QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
DB 481 GGTAGT-----GAATGTGAACCTGGATTCTTTCGGAATGGTACATCCTTGCCATCACA 534

QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB 535 TCATTCTTGGAAATTCGTATCCAGTCACTCTTAGTCGCTTATTTCAACATGAATATTTAT 594

QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
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DB 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
DB 715 TCTGCATCGACAGAGTCTCTGCATCCTTTCATTTCAGAGAGACAGAGGAGAAGAGTAGT 774

QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280
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DB 835 TTCCTCCCAATCAGATCTGTAGCTCTTCCACCAAGGGAAACATGTTGAACTGCTTAGAGCC 894
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QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGAGATTAGCCCAAGTCACTGGCCATCTCTTAGGGGTTTTTCTGCTGTTTGGCTGCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAATTGCTCTTTCATTTTATCTCTCAGCAACAGCTCTTAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPropheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGCACAGCGCTTCAAAAGGCTTCTTGAAATATTTTGTATAAAAAGCAA 1134
QY 381 ProAlaProSerGln--ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCACACACAGCTGGTCAATATCTTCT 1170
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## RESULT 12

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US-10-272-983-13
; Sequence 13, Application US/10272983
; Publication No. US20030148450A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Dang, Huong T.
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lin, I-Lin
; TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors
; FILE REFERENCE: AREN0050
; CURRENT APPLICATION NUMBER: US/10/272,983
; PRIOR FILING DATE: 2002-10-17
; PRIOR APPLICATION NUMBER: US/09/417,044
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,851
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/123,946
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-272-983-13
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## Alignment Scores:

Pred. No.:	4,25e-145	Length:	1173
Score:	1403.50	Matches:	271
Percent Similarity:	79.34%	Conservative:	40
Best Local Similarity:	69.13%	Mismatches:	78
Query Match:	68.63%	Indels:	3
DB:	15	Gaps:	2

US-10-626-126-9 (1-391) x US-10-272-983-13 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

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Db 1 ATGCCAGATACATAATAGCACAATCAATTTATCATAAGCACTCGTGTACTTTAGCATTT 60
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATGCTAGGAATGCTTGGTCATTTAGCTTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAAACCTTAGACATCGAAGTAGTTATTTTCTTAACCTGGCATCTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTTCTTTGGTGGTGTGATCTCCATTCCTTTGTATCATCCCTCACACGCTGTTGCAATGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAATCTGTGTTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATAAATGCTCTCATCATGATGATCGATAGCTGTCAGTCTCAATGCTGCTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATACCTGGGTCTTGAAGATTGTTACTCTGATGGTGGCGTTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160
Db 421 GTGCTGGCCTTCTTAGTGAATGGCCCAATGATCTTAGTTTCAGAGTCTTGGAAAGATGAA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTCAACTGGATTTTTCGGAATGGTACATCCTTGCATCACA 534
QY 181 AlaPheLeuGluPheLeuLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTTAT 594
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCTGTGGAGCGTGATCATCTCAGTAGTGCCAAAGCCATCCTGGAGCTGACTGCT 654
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGCACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714
QY 241 ProGlyLeuLysGluProAlaAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260
Db 715 TCTGCATCGACAGAAGTTCCTGCATCCTTTTCATTCAGAGAGACAGAGAGAGTAGT 774
QY 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleAlaPheLysValGlySer 280
Db 775 CTCATGTTTCTCAAGAACCAAGATGAATAGCATACATTAATGCTTCCAAATGGGTTC 834
QY 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCCACAAAAGGGAACATGTTGAACCTGCTTAGAGCC 894
QY 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCCAAGTCACTGGCCATTCCTTAGGGGTTTTTCTGCTGCTGGGTCCA 954
QY 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTCACAATGCTCTTTTCAATTTTATTCCTCAGCAACAGCTCTTAATCAGTT 1014
QY 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnPropheLeuTyr 360
Db 1015 TGGTATAGAAATGCAATTTGGCTTCAGTGGTTCAAATTCCTTTGTCAATCTCTTTGTAT 1074
QY 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
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Db 1075 CCATTGTGTCAACAGCGCTTTCAAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAA 1134

Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391

Db 1135 CCTCTACCATCAACACAGACGTCGGTCAGTATCTTCT 1170

RESULT 13

US-10-354-769-1

Sequence 1, Application US/10354769

Publication No. US20030149242A1

GENERAL INFORMATION:

APPLICANT: Pfizer Inc.

APPLICANT: O'Reilly, Mark A.

APPLICANT: Peter, Beate

TITLE OF INVENTION: NOVEL POLYPEPTIDE

FILE REFERENCE: PC10373B

CURRENT APPLICATION NUMBER: US/10/354,769

PRIOR FILING DATE: 2003-01-30

PRIOR APPLICATION NUMBER: US 09/698,801

PRIOR FILING DATE: 2000-10-27

PRIOR APPLICATION NUMBER: US 60/211,243

PRIOR FILING DATE: 2000-06-14

PRIOR APPLICATION NUMBER: GB 9925641.4

PRIOR FILING DATE: 1999-10-29

PRIOR APPLICATION NUMBER: GB 0009973.9

PRIOR FILING DATE: 2000-04-20

NUMBER OF SEQ ID NOS: 10

SOFTWARE: PatentIn version 3.1

SEQ ID NO 1

LENGTH: 1173

TYPE: DNA

ORGANISM: Homo sapiens

US-10-354-769-1

Alignment Scores:

Pred. No.: 4,25e-145 Length: 1173

Score: 1403.50 Matches: 271

Percent Similarity: 79.34% Conservative: 40

Best Local Similarity: 69.13% Mismatches: 78

Query Match: 68.63% Indels: 3

DB: 15 Gaps: 2

US-10-626-126-9 (1-391) x US-10-354-769-1 (1-1173)

Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20

Db 1 ATGCCAGATCAATTAAGCACAATCAATTTATCACTAAGCACTCGGTGTTACTTTAGCATTT 60

Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40

Db 61 TTTATGTCCTTAGTAGCTTTTCTATATAGCTAGGAAATGCTTTGGTCATTTTAGCTTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60

Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATATTTTCTTAACCTGGCCATCTCT 180

Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80

Db 181 GACTTCTTTGGGGTGTGATCTCCATTCCTTTGTATACATCCCTCACACGCTGTTCGAATGG 240

Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100

Db 241 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTATACGCA 300

Qy 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120

Db 301 TCTGTATATACATTTGCTCATCAGCTATGATCATCTGCTGAGTCTCAAAATGCTGTG 360

Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTrp 140

Db 361 TCTTATAGAACTCAACATCTAGGGTCTTGAGATGTTTACTCTCATGATGGTGGCGGTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpLysAsnSer 160

Db 421 GTGCTGGCGCTTCTTAGTGAATGGCCAATGATTTCTAGTTTCAGAGTCTTTCGAAGGATCAA 480

Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTrpTyrIleLeuAlaIleThr 180

Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTTTTGGGAATGGTACATCTCTTGGCCATCACA 534

Qy 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200

Db 535 TCATTTCTTGGAAATTCGTGATCCAGTCACTTAGTCGCTTATTTCAACATGAATATTTAT 594

Qy 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220

Db 595 TGGAGCCTGTGGAGCGTGATCACTCTAGTAGTGCCAAAGCCATCTCTGGAGTACTGCT 654

Qy 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240

Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTCAGAGGTAGACTATCTTCAAGGAGATCTCTT 714

Qy 241 ProGlyLeuLysGluProAlaSerLeuHisSerGluSerProArgGlyLysSerSer 260

Db 715 TCTGCATCGACAGAGTTCTCTGCTATCTTCTTTCAGAGACAGAGGAGAAAGATGAT 774

Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheLysValGlySer 280

Db 775 CTCATGTTTTCTCAAGAAACCAAGATGAATAGCAATCAATTCCTTCCAAATGGGTTCC 834

Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300

Db 835 TTCTCCCAATCAGATTCCTGTAGCTCTTCCACCAAGGGAACATGTTGAACTGCTTAGAGCC 894

Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320

Db 895 AGGATTTAGCCAGTCACTGCTCATCTCTTAGGGGTTTTTCTGTTTCTGGGCTTCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340

Db 955 TATTCCTCTGTTCCACAATTTGCTTTTCAATTTTATTCCTCAGCAACAGGTCCTAAATCAGTT 1014

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360

Db 1015 TGGTATAGAATTCGATTTTGGCTTTCAGTGGTTCATTCCTTTGTCATCTCTTTTGTAT 1074

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380

Db 1075 CCATTTGTGTCAAGCGCTTTCAAAGGCTTTCTTGAATAATATTTTGTATATAAAGCAA 1134

Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391

Db 1135 CCTCTACCATCAACACAGTCGGTCAGTATCTTCT 1170

RESULT 14

US-10-393-807-13

Sequence 13, Application US/10393807

Publication No. US20030175891A1

GENERAL INFORMATION:

APPLICANT: Chen, Ruoping

APPLICANT: Dang, Huong T.

APPLICANT: Liaw, Chen W.

APPLICANT: Lin, I-Lin

TITLE OF INVENTION: Human Orphan G Protein Coupled Receptors

FILE REFERENCE: AREN0050

CURRENT APPLICATION NUMBER: US/10/393,807

CURRENT FILING DATE: 2003-03-21

PRIOR APPLICATION NUMBER: US/09/417,044

PRIOR FILING DATE: 1999-10-12

PRIOR APPLICATION NUMBER: 60/109,213

PRIOR FILING DATE: 1998-11-20

PRIOR APPLICATION NUMBER: 60/120,416

PRIOR FILING DATE: 1999-02-16

PRIOR APPLICATION NUMBER: 60/121,851

PRIOR FILING DATE: 1999-02-26

PRIOR APPLICATION NUMBER: 60/123,946

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; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,949
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/136,436
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,437
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,439
; PRIOR FILING DATE: 1999-05-28
; PRIOR APPLICATION NUMBER: 60/136,567
; PRIOR FILING DATE: 1999-05-28
; Remaining Prior Application data removed - See File Wrapper or PALM.
; NUMBER OF SEQ ID NOS: 74
; SOFTWARE: PatentIn Ver. 2.1
; SEQ ID NO 13
; LENGTH: 1173
; TYPE: DNA
; ORGANISM: Homo sapiens
US-10-393-807-13

Alignment Scores:
Pred. No.: 4,25e-145 Length: 1173
Score: 1403.50 Matches: 271
Percent Similarity: 79.34% Conservative: 40
Best Local Similarity: 69.13% Mismatches: 78
Query Match: 68.63% Indels: 3
DB: 16 Gaps: 2

US-10-626-126-9 (1-391) x US-10-393-807-13 (1-1173)

QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
1 ATGCCAGATACATAATAGCAATCAATTTATCACTAAGCACTCGTGTACTTTAGCAATTT 60
QY 21 LeuMetSerLeuAlaPheAlaThrIleGlyAsnAlaValValIleLeuAlaPhe 40
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
61 TTTATGCTCTAGTACTTTCTATTAATGCTAGGAATGCTTTGCTCAATTTAGCTTTT 120
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTATTTTCTTAACCTTGCCATCTCT 180
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTyr 80
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
181 GACTTCTTTGTGGTGTGATCTCCATTCCTTTGTATCATCCCTCACACGCTGTTGCAATGG 240
QY 81 AsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCysThrAla 100
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
241 GATTTTGGAAAGGAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
301 TCTGTATATAACATGTCTCTCATCAGCTATGATGATACCTGTCACTCTCAATGCTGTG 360
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAlaValTyr 140
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
361 TCTTATAGAACCTCAACATACGCGGTCTTGAAGATTTTACTCTGATGGTGGCGGTGG 420
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTyrIleAsnSer 160
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
421 GTGCTGGCCCTCTTAGTGAATGGCCCAATGATCTAGTTTTCGGAATGGTACATCCTGCCATCACA 480
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrIleLeuAlaIleThr 180
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCCTGCCATCACA 534
QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
535 TCATCTTGGAAATTCGTGATCCAGTCATCTAGTCGCTATTTCACATGAATATTTAT 594
QY 201 TrpSerLeuTyrIleArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db |||:||||| ||| |||:||||| |||:||||| |||:||||| |||:|||||
595 TGGAGCCTGTGGAAGCGTGATCATCTCTCAGTAGGTGCCAAAGCCATCCTGGACTGTGCT 654
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## RESULT 15

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US-10-417-820A-13
; Sequence 13, Application US/10417820A
; Publication No. US20030229216A1
; GENERAL INFORMATION:
; APPLICANT: Chen, Ruoping
; APPLICANT: Liaw, Chen W.
; APPLICANT: Lowitz, Kevin
; APPLICANT: Chalmers, Derek T.
; APPLICANT: Behan, Dominic P.
; TITLE OF INVENTION: Constitutively Activated Human G Protein Coupled
; TITLE OF INVENTION: Receptors
; FILE REFERENCE: 7.US28.CON
; CURRENT APPLICATION NUMBER: US/10/417,820A
; PRIOR FILING DATE: 2003-04-16
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/416,760
; PRIOR FILING DATE: 1999-10-12
; PRIOR APPLICATION NUMBER: 09/170,496
; PRIOR FILING DATE: 1998-10-13
; PRIOR APPLICATION NUMBER: 60/110,060
; PRIOR FILING DATE: 1998-11-27
; PRIOR APPLICATION NUMBER: 60/120,416
; PRIOR FILING DATE: 1999-02-16
; PRIOR APPLICATION NUMBER: 60/121,852
; PRIOR FILING DATE: 1999-02-26
; PRIOR APPLICATION NUMBER: 60/109,213
; PRIOR FILING DATE: 1998-11-20
; PRIOR APPLICATION NUMBER: 60/123,944
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,945
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,948
; PRIOR FILING DATE: 1999-03-12
; PRIOR APPLICATION NUMBER: 60/123,951
; PRIOR FILING DATE: 1999-03-12
; Remaining Prior Application data removed - See File Wrapper or PALM.
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/ NUMBER OF SEQ ID NOS: 155  
/ SOFTWARE: PatentIn version 3.2  
/ SEQ ID NO 13  
/ LENGTH: 1173  
/ TYPE: DNA  
/ ORGANISM: Homo sapiens  
US-10-417-820A-13

Alignment Scores:  
Pred. No.: 4.25e-145 Length: 1173  
Score: 1403.50 Matches: 271  
Percent Similarity: 79.34% Conservative: 40  
Best Local Similarity: 69.13% Mismatches: 78  
Query Match: 68.63% Indels: 3  
DB: 17 Gaps: 2

US-10-626-126-9 (1-391) x US-10-417-820A-13 (1-1173)

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Qy 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
Db 1 ATGCCAGATACATATAGCACATCATATATACATAGCACTCGTGTTACTTTAGCATTT 60

Qy 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
Db 61 TTTATGTCCTTAGTAGCTTTTGTATATATGCTAGGAAATGCTTTGTCATTTAGCTTTT 120

Qy 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
Db 121 GTGGTGGACAAACCTTAGACATCGAAGTAGTATTTTCTTAACTTGGCCATCTCT 180

Qy 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
Db 181 GACTCTTTTGGTGGTGTGATCTCCATCTCTTTGTACATCCCTCACACGCTGTTGAAATGG 240

Qy 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
Db 241 GATTTTGGAAAGGAAATCTGTGTATTTTGGCTCACTACTGACTATCTGTATGTACAGCA 300

Qy 101 SerValTyrSerIleValIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
Db 301 TCTGTATATACATTGCTCCTCATCAGCTATGATCATGATACCTGTGTCAGTCTCAAAATGCTGTG 360

Qy 121 ArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGlnMetValAlaValTrp 140
Db 361 TCTTATAGAACTCAACATCTGGGCTCTGAAGATTGTTACTCTCATGTGGCCCTTTGG 420

Qy 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIysAsnSer 160
Db 421 GTGCTGGCCTCTTATAGTGAATGGGCAATGATTCTAGTTTCAGAGTCTTGGGAAGGATGAA 480

Qy 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTrpTyrIleLeuAlaIleThr 180
Db 481 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTATCATCTTGGCCATCACA 534

Qy 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
Db 535 TCATCTTTGGAAATTCGTGATCCCATCTCTTAGTCGCTTATTTCAACATGATATTTAT 594

Qy 201 TrpSerLeuTrpIysArgIysLeuSerArgCysProSerHisAlaGlyPheIleAla 220
Db 595 TGGAGCCTGTGGAGCGTGATCATCTCAGTAGTGCCAAAGCCATCCTGGACTGCTGCT 654

Qy 221 ThrSerSerArgGlyThrGlyHisSerArgThrGlyLeuAlaCysArgThrSerLeu 240
Db 655 GTCTCTTCCAAACATCTGTGGACACTCATTTCAAGAGTAGACTATCTCAAGGAGATCTCTT 714

Qy 241 ProGlyLeuIysGluProAlaAlaSerLeuHisSerGluSerProArgGlyIysSerSer 260
Db 715 TCTGCATCGACAGAGAGTTCTGCTCTTCTTATTCAGAGAGACAGGAGAGAGTAGT 774

Qy 261 LeuLeuValSerLeuArgThrHisMetSerGlySerIleIleAlaPheIysValGlySer 280
Db 775 CTCATGTTTTTCTCAAGAACCAAGATGAATAGCAATACAAATTTGCTTCCAAATGGGTTCC 834
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Qy 281 PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgGly 300
Db 835 TTCTCCCAATCAGATTCTGTAGCTCTTCAACCAAGGGAAACATGTGAACCTCTTAGAGCC 894

Qy 301 ArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPro 320
Db 895 AGGAGATTAGCCAAGTCACTGGCCATCTCTTAGGGGTTTTTGTGTTGCTGGGCTCCA 954

Qy 321 TyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIle 340
Db 955 TATTCTCTGTTTCACAATTGTCTTCTTATTTATTTATTTCTCAGCAACAGGCTCTTAATCAGTT 1014

Qy 341 TrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTyr 360
Db 1015 TGGTATAGAATTGCAATTTTGGCTTCAGTGGTTCAATCTTGTCAATCTCTTTTGTAT 1074

Qy 361 ProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeuCysValThrLysGln 380
Db 1075 CCATTGTGTCAAGGCTTTCAAAAGGCTTTCTTGAATAATTTTGTATAAAAGGCAA 1134

Qy 381 ProAlaProSerGln---ThrGlnSerValSerSer 391
Db 1135 CCTCTACCATCAACAACAGACAGTCGGTCAGTATCTTCT 1170
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Search completed: August 5, 2005, 17:38:06

Job time : 723 secs

GenCore version 5.1.6  
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OM protein - protein search, using sw model

Run on: August 3, 2005, 01:38:32 ; Search time 41 Seconds  
(without alignments)  
917.579 Million cell updates/sec

Title: US-10-626-126-9  
Perfect score: 2045  
Sequence: 1 MSESNGTDVLP LTAQVPLAF.....WKILCVTKQAPSPQTSQSVSS 391

Scoring table: BLOSUM62  
Gapop 10.0 , Gapext 0.5

Searched: 283416 seqs, 96216763 residues  
Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0  
Maximum DB seq length: 2000000000  
Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Database : PIR 79:.\*  
1: pir1:.\*  
2: pir2:.\*  
3: pir3:.\*  
4: pir4:.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	1403.5	68.6	390	JC7566	histamine H4 recep
2	410.5	20.1	590	S47572	muscarinic acetyl
3	408.5	20.0	590	S01114	muscarinic acetyl
4	407.5	19.9	589	A29476	muscarinic acetyl
5	403.5	19.7	590	S10128	muscarinic acetyl
6	401.5	19.6	491	A41632	histamine H1 recep
7	401	19.6	531	JT0531	muscarinic acetyl
8	397.5	19.4	589	B29514	muscarinic acetyl
9	395.5	19.3	487	JC2495	histamine H1 recep
10	395	19.3	532	JT0530	muscarinic acetyl
11	390.5	19.1	386	A42688	serotonin receptor
12	389.5	19.0	460	A24325	muscarinic acetyl
13	389	19.0	639	A55019	muscarinic acetyl
14	388.5	19.0	460	S09508	muscarinic acetyl
15	388	19.0	501	T18863	hypothetical prote
16	387.5	18.9	386	S18637	serotonin receptor
17	387.5	18.9	390	JN0268	serotonin receptor
18	385.5	18.9	460	I51837	muscarinic recepto
19	385.5	18.9	460	A29514	muscarinic acetyl
20	383	18.7	486	JC1415	histamine H1 recep
21	382.5	18.7	488	I56507	histamine H1 recep
22	380.5	18.6	386	S54153	serotonin receptor
23	377	18.4	501	JH0447	alpha-1A-adrenergi
24	377	18.4	572	JT1323	alpha-1A-adrenergi
25	375.5	18.4	477	S71323	serotonin receptor
26	374.5	18.3	389	S68422	alpha-1A-adrenergi
27	374.5	18.3	560	A38731	alpha-1A-adrenergi
28	373.5	18.3	460	A31897	muscarinic acetyl
29	372.5	18.2	515	A40491	alpha-1-adrenergi

30	369.5	18.1	390	2	S58126	serotonin receptor
31	368.5	18.0	517	2	A45121	alpha-1B-adrenergi
32	363.5	17.8	366	2	A47385	serotonin receptor
33	362.5	17.7	515	2	JC1525	alpha-1B-adrenergi
34	361.5	17.7	379	2	JC6178	serotonin receptor
35	361	17.7	466	2	S10126	muscarinic acetyl
36	359	17.6	377	2	A53279	serotonin receptor
37	358.5	17.5	366	2	S26048	serotonin receptor
38	358.5	17.5	479	2	S33776	muscarinic acetyl
39	357.5	17.5	366	2	A47321	serotonin receptor
40	357.5	17.5	429	2	S65656	alpha-1C-adrenergi
41	357.5	17.5	466	2	JN0765	alpha-1C-adrenergi
42	357.5	17.5	466	2	S10856	muscarinic acetyl
43	357.5	17.5	499	2	S65657	alpha-1C-adrenergi
44	356.5	17.4	466	2	A40972	muscarinic acetyl
45	356	17.4	377	2	B30341	G protein-coupled

ALIGNMENTS

RESULT 1

JC7566  
histamine H4 receptor, HH4R - human  
C:Species: Homo sapiens (man)  
C:Date: 30-Jun-2001 #sequence\_revision 30-Jun-2001 #text\_change 09-Jul-2004  
C:Accession: JC7566  
R:Nakamura, T.; Itadani, H.; Hidaka, Y.; Ohta, M.; Tanaka, K.  
Biochem. Biophys. Res. Commun. 279, 615-620, 2000  
A:Title: Molecular cloning and characterization of a new human histamine receptor, HH4R.  
A:Reference number: JC7566; MUID: 20568725; PMID:11118334  
A:Contents: Leukocyte  
A:Accession: JC7566  
A:Molecule type: mRNA  
A:Residues: 1-390 <NAK>  
A:Cross-references: UNIPROT:Q9H3N8; DDBJ:AB045370  
C:Comment: This receptor, belonging to the biogenic amine receptors of G protein-coupled  
C:Genetics:  
A:Gene: hh4r  
C:Keywords: G protein-coupled receptor; transmembrane protein

Query Match	68.6%	Score	1403.5	DB	2	Length	390
Best Local Similarity	69.1%	Pred. No.	7.4e-112				
Matches	271	Conservative	40	Mismatches	78	Indels	3
Gaps							2
Qy	1	MSESNGTDVLP LTAQVPLAF LMSLLAF AITIGNAVVILAFVADRNLRHRSNYFFLNLAIS	60				
Db	1	MPDTNSTINLSLSTRVT LAFPMVSLVAFALMGNALVILAFVVDKRLHRSSYFFLNLAIS	60				
Qy	61	DFPVGVISIPLYIPHTLFNNPGSGICMPWLITDYLLCTASVYSIVLISYDRYOSVSNV	120				
Db	61	DFPVGVISIPLYIPHTLFNWDGKICVFWLTDTLLCTASVYNIVLISYDRYLSVSNV	120				
Qy	121	RYRAOHTGILKVAQVAVVILAFVNGPMILASDSWKSNSTNTECEPGVTVTWYLLAIT	180				
Db	121	SVRTQHTGVLKIVTLVAVVAVLAFVNGPMILVSESKDEGS--ECEPGFSEWYLLAIT	178				
Qy	181	AFLEFLLPSLVVYFVQVYWSLWKRGSLSRCPSHAGFIATSSRGTHSRRTGLACRTSL	240				
Db	179	SFLEFVPIVLVAFVFNWYWSLWKDHLSCOSHFGLTAVSSNICGHSFGRLLSRSL	238				
Qy	241	PGLKEPAALHSGSPRGKSLVSLRTHMSGSIIFAPKVGSCFCSGSPVLHOREHVELLRG	300				
Db	239	SASTEVPAGFHSRQRKSGSLMFSRRTKWSNTIASKMGFSQSDSVALHOREHVELLRA	298				
Qy	301	RKLARSIALVLSAFACWAPYCLFTIVLTYSYRGERPKSIWYSIAFWLQWNSLIMPFLY	360				
Db	299	RLAKSLAILLGVFAVCWAPYSLFTIVLSFYSGATPKSVWYRIAPFWLQWNSFVNPLLY	358				
Qy	361	PLCHRRFQKAFWKILCVTKQAPSQ--TQSVSS 391					
Db	359	PLCHKRFQAKFLKIFCIKKQPLPSQHSRSVSS 390					



F;195-207/Domain: transmembrane #status predicted <TM>  
F;231-252/Domain: transmembrane #status predicted <TM>  
F;493-513/Domain: transmembrane #status predicted <TM>  
F;525-546/Domain: transmembrane #status predicted <TM>  
F;5,6,15,41/Binding site: carbohydrate (Asn) #status predicted

```

Query Match          19.7%; Score 403.5; DB 2; Length 590;
Best Local Similarity 24.3%; Pred. No. 1.6e-26;
Matches 131; Conservative 85; Mismatches 163; Indels 161; Gaps 19;
```

QY	2	SESGNTDVLPLTAQ----	VPLAFLMSLLAFATTIGNAVVILAFVADRNLRHRSNYFFLN	56
DB			: : :	
QY	50	SSPDGTTDDPLGGHTVMQVVFI	AFLTGILALVTIIGNILVFVKMKRUKTVNNYFELS	109
DB			: : :	
QY	57	LAIISDFPVGVGISIPLYPHLTFN-	WNPGSIGICMFWLITDYLLCTASYSIVLSIDRYQS	115
DB			: : :	
DB	110	LACADLIIGVISMNLFTYIIIMNRWALGNLC	DWLALDIVASNASYMNLNVISFDYVFS	169
QY	116	VSNVARYRAQHTGILKIVAQNVA-	NILAFLVNGPMILASDSW-----KNSTWERCEPG	169
DB		: :	: :       : :	
DB	170	ITRPLTYRAKRT--TKRAGVMIGLA	WISFVLWAPAIL---FWQYFVGKRTVPPEGCFIQ	224
QY	170	FVTEWILAITALEFLPLLPSLVVVS	VOIYWSLWKR-----	206
DB			: :	
DB	225	FLSEPITFTGTAAFPMPVTIMTI---	LYRIYKETERTKELAGLASQTGAETENF	280
QY	207	----GSLSRCPFS-----	HAGF-----	218
DB				
DB	281	VHTGSSRSSCSYELOOQSMKRNRKYGRCH	FWFTTKSWKPSEQMDQHSSSDSNNN	340
QY	219	-IATSRGTHGHSRRRTGLACTT-	-----SLPG-----	242
DB				
DB	341	DAASALESNASDEEDIGSETRAIYSIVLK	PLPGHSTILNSTKLPPSSDNLQVPBEELGMVD	400
QY	243	LKEPAASLHSES-----	PRCKSSLVLSLR-----THMSGSI-----IAFKV	278
DB			: : :	
DB	401	LERKADKLQAQSKVDGSGSPFSKLPUIQES	SAVDTAKTSDNVNSVGKSTATLPLSFKE	460
QY	279	GS-----FCRSESPVLHOREHVELLGR	KLARSLAVILSAFAIWAPCYCLFTVLSTVRRG	334
DB			: :	
DB	461	ATLAKRFALKTRSQITPKRMKSLVKEKA	QAOTLSAILAFIITWPYNIMVLV-NTFCD	519
QY	335	ERPKSIIWYSTAFWLQFNLSLINPFLYPLC	HRRFRQKAFWKIL---CVTKQPAPSGQTQSVSS	391
DB			: :	
DB	520	CIPKTFW-NLGWMLCYINSTVNPVCVALCN	KTKTFTFMKLLQCQDKKKRKQQYQQRQS	578

RESULT 6  
A41632  
histamine H1 receptor - bovine  
C:Species: Bos primigenius taurus (cattle)  
C>Date: 28-Aug-1992 #sequence\_revision 28-Aug-1992 #text\_change 09-Jul-2004  
C:Accession: A41632  
R:Yamashita, M.; Fukui, H.; Sugama, K.; Horio, Y.; Ito, S.; Mizuguchi, H.; Wada  
Proc. Natl. Acad. Sci. U.S.A. 88, 11515-11519, 1991  
A>Title: Expression cloning of a cDNA encoding the bovine histamine H-1 receptor  
A:Reference number: A41632; MUID:92107981; PMID:1722337  
A:Accession: A41632  
A>Status: preliminary  
A:Molecule type: mRNA  
A:Residues: 1-491 <YAM>  
A:Cross-references: UNIPROT:P30546; GB:D10197; GB:D90430; NID:g217569; PIDN:BAA  
C:Superfamily: vertebrate rhodopsin  
C:Keywords: G protein-coupled receptor; transmembrane protein

```

Query Match          19.6%; Score 401.5; DB 2; Length 491;
Best Local Similarity 24.8%; Pred. No. 2e-26;
Matches 123; Conservative 82; Mismatches 148; Indels 143; Gaps 18;
```

QY	1	MSSNGTDDLPLTAQVPLAFLMSLLAFATTIG-	NAVVILAFVADRNLRHRSNYFFLN	59
DB			: :	
DB	14	MCQGNTKAPANDAQLTPLVVVLSTISU-VTV	GNLNLVLYVRSEKLUHTVGNVLSLSV	72





Biochem. Biophys. Res. Commun. 197, 1601-1608, 1993

A;Title: Genomic cloning, heterologous expression and pharmacological characterization of  
A;Reference number: JC2035; MUID:94107375; PMID:8280179

A;Accession: JC2035

A:Molecule type: DNA

A;Residues: 1-487 <DB>

A;Cross-references: GB:G76786; NID:g442517; PIDN:CAA54182.1.; PID:g442518

R;Mogulilevsky, N.; Varsalona, F.; Noyer, M.; Gillard, M.; Guillaume, J.P.; Garcia, L.; S;  
Eur. J. Biochem. 224, 489-495, 1994

A;Title: Stable expression of human H(1)-histamine-receptor cDNA in Chinese hamster ovary  
localisation of the gene.

A;Reference number: S48144; MUID:95010026; PMID:7925364

A;Accession: S48144

A;Status: preliminary

A:Molecule type: mRNA

A;Residues: 1-487 <MOG>

A;Cross-references: EMBL:Z34897; NID:g510295; PIDN:CAA84380.1.; PID:g510296

C;Comment: This receptor mediates the increase in capillary permeability through immune-f

C;Genetics:

A;Gene: GDB:HRH1

A;Cross-references: GDB:303929; OMIM:600167

A;Map position: 3p21-3p14

C;Superfamily: vertebrate rhodopsin

C;Keywords: Glycoprotein; phosphoprotein; receptor; transmembrane protein

F;30-49/Domain: transmembrane #status predicted <TM1>

F;64-83/Domain: transmembrane #status predicted <TM2>

F;102-121/Domain: transmembrane #status predicted <TM3>

F;136-165/Domain: transmembrane #status predicted <TM4>

F;190-209/Domain: transmembrane #status predicted <TM5>

F;419-438/Domain: transmembrane #status predicted <TM6>

F;451-470/Domain: transmembrane #status predicted <TM7>

F;5.18/Domain site: carbohydrate (Asn) (covalent) #status predicted

F;107,194,198/Binding site: histamine (Asp, Thr, Asn) #status predicted

F;128,235,255,378,396,398/Binding site: phosphate (Ser) (covalent) (by protein kinase C)

F;140,142,390,478/Binding site: phosphate (Thr) (covalent) (by protein kinase C) #status

Query Match 19.3%; Score 395.5; DB 2; Length 487;  
Best Local Similarity 24.8%; Pred. No.6.4e-26;  
Matches 120; Conservative 80; Mismatches 161; Indels 123; Gaps 16;

Qy 1 MSSENGTDVPLTAQVLAFLMSLLAFATITG-NAVWILAFVADRNLRHSNVFFNLAI 59  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
14 MCEGNKT-TWASPOLMPLVVVLSTICL-VTVGLNLLVLYAVRSEKRLHTVGNYLVSLSV 71  
Qy 60 SDPFVGVISPLYIPTHLEFN-WNPESGICMEFWLITDYLLCTASVYSIVLISVDYQSVEN 118  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
72 ADLIVGVMPNNLYLLMSKWSLGRPCLFSLWSMDYVASTASIFSIFLCIDRYRSVOQ 131  
Qy 119 AVRYRAQTGTLKIVAQVAWVILAFLVNGFMILASDSWKQNSTNT---ECEPGFVTEWY 175  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
132 PLRYLKVRTK-TRASATILGAWELSFLLWVIP-ILGNHFMMQOTSVRREDKCTDFDYVTW 189  
Qy 176 ILAITAFLEPLLVSIVYFSVQIY----- 200  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
190 FKVMATAINFPYLTLMLWFYAKIYKAVROHCQHRELINRSLPSFSEIKLRPENPKGDAAK 249  
Qy 201 -----WSLWKR-----GSLSRCPSHA-----GFIA 220  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
250 KPGKESPEWLKRPKDAAGGSVJLKSQTPKEMKSPVVFQSDDEDDREVDKLVCFFPLDIHV 309  
Qy 221 TSSRGTHSR-----RTGLACRTLSPGLKEPAAS-----LHSES 254  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
310 MQAAAEGSRRDYYAVNRSHGQLKTDQGLNTHGASEISEIQMLGDSQSFRTSDTDTTET 369  
Qy 255 PRGSKSLLVSLRTHMSGSIITAFKVSGFCRCSPPVLHQREHVELL---RGRKLARSLAVUL 311  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
370 APGGKGLRSGSNTGLDIYKFTWK-----RLRS--HSRQYVSGLHMNRERKAQQLGFTM 421  
Qy 312 SAFAI CWAPCYCLFTIVLSTYRGERPKSIWIYSIAFWLOWFNSLINPFLYPLCHRFQAKF 371  
Db ||| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :|| :||  
422 AAFILCWIPFIPIPMWIAFCNCKNEHLHMTETI---WLGVIINSTLNPLIYPLCNENFKKTF 479  
Qy 372 WKIL 375



C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:25-50/Domain: transmembrane #status predicted <TM1>  
F:62-93/Domain: transmembrane #status predicted <TM2>  
F:100-121/Domain: transmembrane #status predicted <TM3>  
F:142-168/Domain: transmembrane #status predicted <TM4>  
F:187-209/Domain: transmembrane #status predicted <TM5>  
F:367-387/Domain: transmembrane #status predicted <TM6>  
F:402-420/Domain: transmembrane #status predicted <TM7>

Query Match 19.0%; Score 389.5; DB 2; Length 460;  
Best Local Similarity 27.5%; Pred. No. 1.9e-25;  
Matches 119; Conservative 80; Mismatches 161; Indels 73; Gaps 17;

QY 5 NGTDVLPPLTAQVPLAFL---MSLLAFATIGNAVILAFVADRLNLRHRYNFFLNLAISD 61  
DB 12 NITVLAPGKPMQVAFIGITGLLSLATVTGNLLVLSFKVATELKTANNVYFLLSLACAD 71  
QY 62 FVGVGISIPLYIPHTLFL-NNPQSGICMFWLITDYLCTASVYIVLSVDRVQSVNAV 120  
DB 72 LIIGTFMNLVYTYLLMGHWLGTACDLWLADLYVASNVNLLLSFDYFYSVTRPL 131  
QY 121 RYRAQHTGILKIVAOVAV-WILAFVNGPMILASDSW-----KNSNTTECEPEPGFVTEW 174  
DB 132 SYRAKRP--RRAALMIGLAWLSFVLWAPAIL---FWOYLGERVTLAQCVYQLSQP 186  
QY 175 YILAITAFLEPLVSLVYVFSQIYVWSLWKR-----GSL--SRCPSHAGFIATSR 224  
DB 187 IITFTGAMAAYFLPVTVM---CTLYWRYIYRETNARELAALQGSFPGKGGSSSSSE 242  
QY 225 ----GTGHSRRT--GLACR-TSLPGLKEPAA-SLHSESPRGKSSLLVSLRTHMSGSIAP 276  
DB 243 RSQPAAGSPETPPGRCRCCRAPRLQAYSWKEEEDGSMESLTSSEGEPEPGSEVVI 302  
QY 277 KYGSP-CRSESPV-----LHOREHVELLRGRK 302  
DB 303 KPMVDPEAQAKQPPRSNPVTKPRKGRERAGKQKPRGKEQLAKRTFSLVKEK 362  
QY 303 LARSVALLSAFAICWAPYCLFTVLSTYRGERPKSIWYSIAFWLQWNSLINPFLYPL 362  
DB 363 AARTLSAILLAFITVTPYINMVLV-STFKCKCVPETLW-ELGYWLCYVNSTINPMCYAL 420  
QY 363 CHRRQKAFWKIL 375  
DB 421 CNKAFRDTFRLLL 433

RESULT 13  
AS5019  
muscarinic acetylcholine receptor, M3 isoform - chicken  
C;Species: Gallus gallus (chicken)  
C;Date: 11-Nov-1994 #sequence\_revision 11-Nov-1994 #text\_change 09-Jul-2004  
C;Accession: A55019  
R;Gadbut, A.P.; Galper, J.B.  
J. Biol. Chem. 269, 25823-25829, 1994  
A;Title: A novel M-3 muscarinic acetylcholine receptor is expressed in chick atrium and  
A;Reference number: A55019; MUID:95014393; PMID:7929287  
A;Accession: A55019  
A;Status: preliminary  
A;Molecule type: mRNA  
A;Residues: 1-639 <GAD>  
A;Cross-references: UNIPROT:P49578; GB:U10617; NID:G530097; PIDN:AAA65961.1; PID:G530098  
A;Superfamily: vertebrate rhodopsin  
C;Keywords: neurotransmitter receptor

Query Match 19.0%; Score 389; DB 2; Length 639;  
Best Local Similarity 24.8%; Pred. No. 3.1e-25;  
Matches 134; Conservative 89; Mismatches 153; Indels 168; Gaps 21;

QY 2 SBSNGTDVLPPLTAQ-----VPLAFMLSLAFATIGNAVVILAFVADRLNLRHRSNYFFLN 56  
DB 98 SSLNATIKDPLGGHAWQVVLIAFLTGIALVTIIGNILVIVSFKNQKLTNNVYFLLS 157  
QY 57 LAISDFVGVVISIPLYIPHTLFL-NNPQSGICMFWLITDYLCTASVYIVLSYDRYQS 115

DB 158 LACADLIIGVISNLTFTTYIINGHWALGNLACDLWLSIDYVASNVMNLLLVISFDYFS 217  
QY 116 VSNVRYRAQHTGILKIVAOVAV-WILAFVNGPMILASDSW-----KNSNTTECEPG 169  
DB 218 ITRPLTYRAKRT--TKRAGVMIGLAWIISFVLWAPAIL---FWOYFVGKRTVPLDSCFIQ 272  
QY 170 FVTEWYILAITAFLEPLVSLVYVFSQIYVWSLWKRGSLSRCPSHAGFIATSSRG---- 225  
DB 273 FLSEPIITFTGATAAFYLPVTIM---SI-LYWRIYKE-TEKRTKELAGLQASGSEATAR 327  
QY 226 ----TCHSRRTG-----LACRTSLPGL----- 243  
DB 328 FVHQGSSSLSSYELQROSTRSSRRKYRCHFWLTKMSWEPNTDQGOEHSSSSWNN 387  
QY 244 KPPAASLHSES-----PRGKSSLLVSLRTHMSGSIAPKV----- 278  
DB 388 NDAASLANSASDEEDITAEITRAIYIVLKLPGH-SAILNSTKLPSSEDLNESADELQK 446  
QY 279 -----GSPCRSES--PV----- 288  
DB 447 SDTDSOEKPKKLQPPKSIQDGSFQKSPSKLPQPSAETATASDGISSVTKTSAALPL 506  
QY 289 -----LHOREHVELLRGRKLARSILAVLSAFAICWAPYCLFTVLST 330  
DB 507 SPKEATLAKKPAKTRSQITTKRMSLIKEKAAQOTLSAILFAFIITWTPYINMVLV-NT 565  
QY 331 YRRGERPKSIWYSIAFWLQWNSLINPFLYPLCHRRFQKAFWKIL---CVTKOPAPSQTQ 387  
DB 566 FDCV-PTVW-NLGWLCYINSTVNPVCYALCNKMFRTFMILLLCQCDKRRKQQYQ 623  
QY 388 SVSS 391  
DB 624 QROS 627

RESULT 14  
S09508  
muscarinic acetylcholine receptor M1 - human  
C;Species: Homo sapiens (man)  
C;Date: 11-Dec-1990 #sequence\_revision 31-Dec-1990 #text\_change 09-Jul-2004  
C;Accession: S09508; S06327; S04326  
R;Chapman, C.G.; Browne, M.J.  
Nucleic Acids Res. 18, 2191, 1990  
A;Title: Isolation of the human m1 (Hml) muscarinic acetylcholine receptor gene by PCR an  
A;Reference number: S09508; MUID:90245684; PMID:2336407  
A;Accession: S09508  
A;Status: nucleic acid sequence not shown; translation not shown  
A;Molecule type: DNA  
A;Residues: 1-460 <CHA>  
A;Cross-references: UNIPROT:P11229; EMBL:X52068; NID:G34450; PIDN:CAA36291.1; PID:G34451  
A;Note: the nucleotide sequence was submitted to the EMBL Data Library, March 1990  
R;Allard, W.J.; Sigal, I.S.; Dixon, R.A.F.  
Nucleic Acids Res. 15, 10804, 1987  
A;Title: Sequence of the gene encoding the human M1 muscarinic acetylcholine receptor.  
A;Reference number: S06327; MUID:88096607; PMID:3697105  
A;Accession: S06327  
A;Molecule type: DNA  
A;Residues: 1-460 <ALL>  
A;Cross-references: GB:Y00508; GB:M35128; NID:G297405; PIDN:CAA68560.1; PID:G297406  
R;Peralta, E.G.; Ashkenazi, A.; Winslow, J.W.; Smith, D.H.; Ramchandran, J.; Capon, D.J.  
EMBO J. 6, 3923-3929, 1987  
A;Title: Distinct primary structures, ligand-binding properties and tissue-specific expre  
A;Reference number: S04326; MUID:88166632; PMID:3443095  
A;Accession: S04326  
A;Molecule type: DNA  
A;Residues: 1-172, 'M', 174-460 <PER>  
A;Cross-references: EMBL:X15263; NID:G32317; PIDN:CAA33334.1; PID:G32318  
C;Superfamily: vertebrate rhodopsin  
C;Keywords: G protein-coupled receptor; glycoprotein; neurotransmitter receptor; phospho  
F:25-50/Domain: transmembrane #status predicted <TM1>  
F:62-93/Domain: transmembrane #status predicted <TM2>  
F:100-121/Domain: transmembrane #status predicted <TM3>



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OM protein - nucleic search, using frame\_plus\_p2n model

Run on: August 5, 2005, 13:53:45 ; Search time 3173 Seconds  
(without alignments)  
4690.554 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

Sequence: 1 MSESNGTDVLPATAQVPLAF.....WKILCVTKQAPSPQTSQSVSS 391

Scoring table:

BLOSUM62  
Xgapop 10.0 , Xgapext 0.5  
Ygapop 10.0 , Ygapext 0.5  
Fgapop 6.0 , Fgapext 7.0  
Delop 6.0 , Delext 7.0

Searched: 34239544 seqs, 19032134700 residues

Total number of hits satisfying chosen parameters: 68479088

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%  
Maximum Match 100%  
Listing first 45 summaries

Command line parameters:

-MODEL=frame+p2n.model -DEV=xlp  
-Q=/cpn2.1/USPTO.spool\_p/US10626126/runat\_02082005\_155436\_2017/app.query.fasta\_1.583  
-DB=EST -QFMT=fastap -SUFFIX=rest -MINMATCH=0.1 -LOOPEXT=0 -LOOPEXT=0  
-UNITS=bits -START=1 -END=1 -MATRIX=blosum62 -TRANS=human40.cdi -LIST=45  
-DOCAUG=200 -THR SCORE=pct -THR MAX=100 -THR MIN=0 -ALIGN=15 -MODE=LOCAL  
-OUTFMT=ptc -NORM=ext -HEAPSIZE=500 -MINLEN=0 -MAXLEN=2000000000  
-USER=US10626126 @CGN 1 1 5180 @runat\_02082005\_155436\_2017 -NCPU=3  
-NO MAP -LARGEQUERY -NEG SCORES=0 -WAIT -DSPBLOCK=100 -LONGLOG  
-DEV TIMEOUT=120 -WARN TIMEOUT=30 -THREADS=1 -XGAPOP=10 -XGAPEXT=0.5 -FGAPOP=6  
-FGAPEXT=7 -XGAPOP=10 -YGAPOP=10 -YGAPEXT=0.5 -DELOP=6 -DELEXT=7

Database :

EST:  
1: gb\_est1:\*  
2: gb\_est2:\*  
3: gb\_hic:\*  
4: gb\_est3:\*  
5: gb\_est4:\*  
6: gb\_est5:\*  
7: gb\_est6:\*  
8: gb\_gss1:\*  
9: gb\_gss2:\*

Pred. No. is the number of results predicted by chance to have a  
score greater than or equal to the score of the result being printed,  
and is derived by analysis of the total score distribution.

#### SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	875	42.8	839	5 BX643713	DKFZp781C
2	857	41.9	704	7 CF147821	AGENCOURT
3	484	23.7	721	7 CO959034	AGENCOURT
4	456.5	22.3	732	7 CF147822	AGENCOURT
5	405	19.6	1773	9 AY400782	Homo sapi
6	401	19.6	672	6 CB556920	AMGNNUC:U
7	397.5	19.4	853	6 CD326085	AGENCOURT
8	397.5	19.4	1770	9 AY400784	Mus muscu
9	397.5	19.4	3171	3 AK080950	Mus muscu

10	392.5	19.2	2780	3	AK032763	Mus muscu
11	392.5	19.2	2831	3	AK047070	Mus muscu
12	392.5	19.2	2979	3	AK038480	Mus muscu
13	392.5	19.2	3783	3	AK046607	Mus muscu
14	390.5	19.1	1161	9	AY415607	Mus muscu
15	387.5	18.9	1173	9	AY415605	Homo sapi
16	384	18.8	3816	3	AK081248	Mus muscu
17	380.5	18.6	1173	9	AY415606	Pan trogl
18	372.5	18.2	1764	3	BC018330	Mus muscu
19	372.5	18.2	2611	3	AK004891	Mus muscu
20	372.5	18.2	3050	3	AK043877	Mus muscu
21	365.5	17.9	1401	9	AY399426	Homo sapi
22	359	17.6	1134	9	AY418218	Homo sapi
23	358.5	17.5	1440	9	AY404936	Mus muscu
24	358.5	17.5	2578	3	AK045364	Mus muscu
25	357.5	17.5	2232	3	CR606112	full-leng
26	356.5	17.4	1125	9	AY418220	Mus muscu
27	356.5	17.4	2908	3	AK082016	Mus muscu
28	354.5	17.3	1440	9	AY404935	Pan trogl
29	352.5	17.2	1203	9	AY407499	Homo sapi
30	352.5	17.2	1440	9	AY404934	Homo sapi
31	351.5	17.2	1072	9	AY398880	Mus muscu
32	351.5	17.2	1401	9	AY399428	Mus muscu
33	351.5	17.2	4124	3	AK085653	Mus muscu
34	351.5	17.2	4135	3	AK079597	Mus muscu
35	347.5	17.0	1072	9	AY398881	Pan trogl
36	343.5	16.8	1203	9	AY407500	Pan trogl
37	340.5	16.7	1069	9	AY398882	Mus muscu
38	337.5	16.5	2410	3	BC035047	Homo sapi
39	334.5	16.4	3594	3	AK046802	Mus muscu
40	333.5	16.3	1335	9	AY418853	Mus muscu
41	333.5	16.3	1347	9	AY416858	Mus muscu
42	330	16.1	1200	9	AY407501	Mus muscu
43	328.5	16.1	1353	9	AY416856	Homo sapi
44	326.5	16.0	1269	9	AY402237	Homo sapi
45	322.5	15.8	1269	9	AY402239	Mus muscu

#### ALIGNMENTS

RESULT 1						
LOCUS	BX643713	839 bp	mRNA	linear	EST 04-SEP-2003	
DEFINITION	DKFZp781C0629_r1 781 (synonym: hlec4) Homo sapiens cDNA clone					
ACCESSION	DKFZp781C0629 5', mRNA sequence.					
VERSION	BX643713					
KEYWORDS	EST.					
SOURCE	BX643713.1 GI:34478046					
ORGANISM	Homo sapiens (human)					
REFERENCE	1 (bases 1 to 839)					
AUTHORS	Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., Oeanger,A., Fobo,G., Han,M. and Wiemann,S.					
TITLE	EST (Lauber,J., Bahr,A., Mewes,H.W., Weil,B., Amid,C., et al.)					
JOURNAL	Unpublished (2003)					
COMMENT	Contact: MIPS					
	MIPS					
	Ingolstaedter Landstr.1, D-85764 Neuherberg, Germany					
	This is the 5' sequence of the clone insert					
	Cloned from S. Wiemann, Molecular Genome Analysis, German Cancer					
	Research Center (DKFZ); Email: s.wiemann@dkfz-heidelberg.de;					
	sequenced by Olagen (Hilden/Germany) within the cDNA sequencing					
	consortium of the German Genome Project.					
	No sl sequence available.					
	This clone (DKFZp781C0629) is available at the RZPD in Berlin.					
	Please contact the RZPD: Ressourcenzentrum, Heubnerweg 6, 14059					
	Berlin-Charlottenburg, GERMANY; Email: clones@rzpd.de.					
FEATURES	Location/Qualifiers					
source	1..839					
	/organism="Homo sapiens"					
	/mol_type="mRNA"					

/db\_xref="taxon:9606"  
/clone="DKFZp781C0629"  
/dev\_stage="adult"  
/lab\_host="DH10B"  
/clone\_lib="781 (synonym: hicc4)"  
/note="Vector: pSport1\_Sfi; Site\_1: SfiIA; Site\_2: SfiIB;  
cDNA-collection"

## ORIGIN

Alignment Scores:  
Pred. No.: 9,65e-76 Length: 839  
Score: 875.00 Matches: 175  
Percent Similarity: 79.9% Conservative: 24  
Best Local Similarity: 70.2% Mismatches: 48  
Query Match: 42.7% Indels: 3  
DB: 5 Gaps: 1

US-10-626-126-9 (1-391) x BX643713 (1-839)

```
QY 1 MetSerGluSerAspGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
96 ATGCCAGATACCTAATAGCACAACTAATTTATCCTAGGACCTCGTGTACTTTAGCATTT 155
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPhe 40
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
156 TTTATGCTCTTAGTAGCTTTGCTATATGCTAGGAATGCTTTGCTCATTTAGCTTTT 215
QY 41 ValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSer 60
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
216 GTGGTGGACAAACCTAGACATCGAAGTAGTATTTTTTTCTTAACCTGGCCATCTCT 275
QY 61 AspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrp 80
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
276 GACTTCTTTGGGTGGTGAATCTCCATCTTTGTCATCTCCCTCACCGCTGTGGAATGG 335
QY 81 AsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeuLeuCysThrAla 100
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
336 GATTTTGGAAAGGAATCTGTGATTTTGGCTCACTACTGACTATCTGTATGTACGCA 395
QY 101 SerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsnAlaVal 120
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
396 TCTGTATATAACATTTGCTCATCATGATGATGATGATGATGATGATGATGATGATG 455
QY 121 ArgTyrArgAlaGlnHisThrGlyIleLeuValIleValAlaGlnMetValAlaValTrp 140
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
456 TCTTATAGAACTCAACATCTGGGTCTTGAAGATTGTTACTCTGAATGGCCGTTGG 515
QY 141 IleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSerTrpIlyAsnSer 160
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
516 GTGCTGGCTCTTAGTGAATGGCCAAATGATCTTAGTTTCAGAGTCTTTGGAAGGATGA 575
QY 161 ThrAsnThrGluGluCysGluProGlyPheValThrGluTyrTyrIleLeuAlaIleThr 180
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
576 GGTAGT-----GAATGTGAACCTGGATTTTTCGGAATGGTACATCTCCCATCACA 629
QY 181 AlaPheLeuGluPheLeuProValSerLeuValValTyrPheSerValGlnIleTyr 200
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
630 TCATTCTTGGAAATTCGTGATCCAGTCATCTTAGTCGCTTATTTCAACATGAATATTAT 689
QY 201 TrpSerLeuTrpLysArgGlySerLeuSerArgCysProSerHisAlaGlyPheIleAla 220
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
690 TGGAGCTTGGAGCGTGATCATCTCAGTAGTGCCAAAGCCATCTCGACTGCTGCT 749
QY 221 ThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeuAlaCysArgThrSerLeu 240
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
750 GTCCTCTCCACATCTGT-GGACACTCAATTCAGAGGTAGACTATCTTCAAGGAGATCTCT 808
QY 241 ProGlyLeuLysGluProAlaAlaSer 249
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
809 TCTGCATCGACAGAGTCTCCTGCATCC 835
```

RESULT 2  
,CF147821

LOCUS CF147821 704 bp mRNA linear EST 25-JUL-2003  
DEFINITION AGENCOURT 14740195 NIH\_MGC\_145 Homo sapiens cDNA clone  
IMAGE:6971900 5', mRNA sequence.  
ACCESSION CF147821  
VERSION CF147821.1 GI:33244089  
KEYWORDS EST.  
SOURCE Homo sapiens (human)  
ORGANISM Homo sapiens  
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
REFERENCE 1 (bases 1 to 704)  
AUTHORS NIH-MGC http://mgc.nci.nih.gov/.  
TITLE National Institutes of Health, Mammalian Gene Collection (MGC)  
JOURNAL Unpublished (1999)  
COMMENT Contact: Daniela S. Gerhard, Ph.D.  
Office of Cancer Genomics  
National Cancer Institute / NIH  
Bldg. 31 Rm10A07 Bethesda, MD 20892  
Email: cgapbs-remail.nih.gov  
Tissue Procurement: GPCR Consortium  
cDNA Library Preparation: GPCR Consortium  
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)  
DNA Sequencing by: Agencourt Bioscience Corporation  
Clone distribution: MGC clone distribution information can be  
found through the I.M.A.G.E. Consortium/LLNL at:  
http://image.llnl.gov  
Plate: IRS102 row: b column: 07  
High quality sequence stop: 685.  
Location/Qualifiers  
1..704  
/organism="Homo sapiens"  
/mol\_type="mRNA"  
/db\_xref="taxon:9606"  
/clone="IMAGE:6971900"  
/tissue\_type="mixed"  
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/clone\_lib="NIH\_MGC\_145"  
/note="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
varies by clone; ORFs were PCR-amplified and cloned into  
pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
clone and include the following: 5'-EcoRV-XmiI/XhoI-3',  
5'-EcoRV-XmiI/NotI-3', EcoRV (TA cloned, non-directional).  
For information about which gene each clones represents,  
please visit our anonymous ftp site at  
ftp://image.llnl.gov/image/rearrayed\_plates/IRBI.presv.dat  
a Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
Pred. No.: 4,4e-74 Length: 704  
Score: 857.00 Matches: 169  
Percent Similarity: 82.13% Conservative: 24  
Best Local Similarity: 71.91% Mismatches: 40  
Query Match: 41.91% Indels: 3  
DB: 7 Gaps: 1

US-10-626-126-9 (1-391) x CF147821 (1-704)

```
QY 3 GluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMet 22
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
5 GATACATAATAGCACAACTAATTTATCCTAGGACCTCGTGTACTTTAGCATTTTATG 64
QY 23 SerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIleLeuAlaPheValAla 42
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
65 TCCTTAGTAGCTTTTGGCTATATGCTAGAAATGCTTTGGTCACTTTAGCTTTTGGTGG 124
QY 43 AspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIleSerAspPhe 62
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
125 GACAAAACCTTAGACATCGAAGTAGTATTTTCTTAACCTGGCCATCTCTGACTTC 184
QY 63 PheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPheAsnTrpAsnPro 82
DB |||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:
185 TTTGTGGGTGTGATCTCCATTCCTTTGTACATCCCTCACACGCTGTTCGAATGGGATTTT 244
```



DNA Sequencing by: Agencourt Bioscience Corporation  
 Clone distribution: MGC clone distribution information can be  
 found through the I.M.A.G.E.B. Consortium/LLNL at:  
<http://image.llnl.gov>  
 Plate: IRB102 row: b column: 06  
 High quality sequence stop: 610.

Location/Qualifiers

1..732  
 /organism="Homo sapiens"  
 /mol\_type="mRNA"  
 /db\_xref="taxon:9606"  
 /clone="IMAGE:6971899"  
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 /clone\_lib="NIH\_MGC\_145"  
 /notes="Vector: pCDNA3.1; Site 1: varies by clone; Site 2:  
 varies by clone; ORFs were PCR-amplified and cloned into  
 pCDNA3.1 by the GPCR Consortium. Cloning sites vary by  
 clone and include the following: 5'-EcoRV-XmnI/XhoI-3',  
 5'-EcoRV-XmnI/NotI-3', EcoRV (TA cloned, non-directional).  
 For information about which gene each clone represents,  
 please visit our anonymous ftp site at  
[ftp://image.llnl.gov/image/rearranged\\_plates/IRB1.presv.dat](ftp://image.llnl.gov/image/rearranged_plates/IRB1.presv.dat)  
 a Note: this is a NIH\_MGC Library."

## ORIGIN

Alignment Scores:  
 Pred. No.: 2.17e-34 Length: 732  
 Score: 456.50 Matches: 95  
 Percent Similarity: 64.47% Conservative: 32  
 Best Local Similarity: 48.22% Mismatches: 59  
 Query Match: 22.32% Indels: 11  
 DB: 7 Gaps: 4

US-10-626-126-9 (1-391) x CF147822 (1-732)

Qy 18 LeuAlaPheLeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValIle 37  
 Db 125 CTGGCGGCTCATGGCGCTGCTCATCTGCGCCAGCGTGTGGGCAACGCGTGTGATG 184  
 Qy 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57  
 Db 185 CTCGCTTGTGTGGCGACTCGAGCGCTCGCCACCCAGAACTTCTTCTGCTCAACCTC 244  
 Qy 58 AlaIleSerAspPheValIleValIleSerIleProLeuTyrIleProHisThrIle 77  
 Db 245 GCCATCTCCGACTTCTCTGTCGGCGCCCTTGTGATCCACCTGTATGATCCCTACGTGCTG 304  
 Qy 78 Phe---AsnTyrAsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyrLeu 96  
 Db 305 ACAGGCGCTGGACCTTTCGGCGGGGCTCTGCAAGCTGTGGTGTAGTGGACTTACCTG 364  
 Qy 97 LeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerVal 116  
 Db 365 CTGTGCACCTCTCTGCTTCAACATCTGCTCATCTCAGTACGACCGCTTCTGTCGGTCT 424  
 Qy 117 SerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMet 136  
 Db 425 ACCGAGCGGTCTCATACCGGGCCAGCAGGGGTGACACGCGCGGGCGAGTCGGGAAGATG 484  
 Qy 137 ValAlaValTyrIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156  
 Db 485 CTGCTGGTGTGGTGTGGCTTCTGCTGTACGAGCAGCCATCTG-----AGC 535  
 Qy 157 TrpLys-----AsnSerThrAsnThrGluGluCysGluProGlyPheVal 171  
 Db 536 TGGAGTACCTGTCCGGGGGAGCTCCATCCCGAGGGCCACTGTATGCGGAGTCTTC 595  
 Qy 172 ThrGluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191  
 Db 596 TACAACTGGTACTTCTTCATCAGCGCTTCCACACTGGAGTGTCTTACCGCCCTCTCAGC 655  
 Qy 192 ValValTyrPheSerValGlnIleTyrTrpSerLeuTyrLysArgGlySer 208

Db 656 GTCACTTCTTTAACTTACCTCACCATTCTACTGAAATC-----AGAGGGCA 700

## RESULT 5

AY400782

LOCUS

DEFINITION

AY400782.1 GI:39756771

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

PUBMED

AUTHORS

TITLE

JOURNAL

COMMENT

FEATURES

source

gene

ORIGIN

Alignment Scores:

Pred. No.: 1.16e-28 Length: 1773

Score: 405.00 Matches: 141

Percent Similarity: 41.71% Conservative: 83

Best Local Similarity: 26.26% Mismatches: 159

Query Match: 19.80% Indels: 155

DB: 9 Gaps: 19

US-10-626-126-9 (1-391) x AY400782 (1-1773)

Qy 2 SerGluSerAsnGlyThrAspValLeuProLeuThrAlaGln-----Val 16

Db 148 TCCCTCCAGACGGTACCACCGATGACCTCTGGAGGTGCATACCGTCTGGCAAGTGTGTC 207

Qy 17 ProLeuAlaPheLeuMetSerLeuAlaPheAlaIleThrIleGlyAsnAlaValVal 36

Db 208 TTCATCGCTTCTTAAACGGGCTCTGCGCTTGTGTGACCATCATCGGCAACATCCTGCTA 267

Qy 37 IleLeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsn 56

Db 268 ATTGTGTCATTAAAGGTCAACAGCAGCTGAAGACGGTCAACAACTACTTCTCTTAAGC 327

Qy 57 LeuAlaIleSerAspPhePheValIleSerIleProLeuTyrIleProHisThr 76

Db 328 CTGGCTGTGGCGATCTGATTATCGGGTCAATTCATGATGATCTTACGACCTACATC 387

Qy 77 LeuPheAsn---TrpAsnProGlySerGlyIleCysMetPheThrLeuIleThrAspTyr 95

Db 388 ATCATGAATCGATGGCGCTTAGGGAACCTGGCTGTGACCTCTGGCTTGCCTTGCATTGAC 447

FEATURES  
 source



```
QY 96 LeuLeuCysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSer 115
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Db 448 GTAGCAGCAATGCTCTGTATGAATCTCTGGTCATCAGCTTTGACAGATACCTTTTCC 507
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QY 116 ValSerAsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuIleValAlaGln 135
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Db 508 ATCAGAGCCCTCAGTACCAGCCCAACAAACA-----ACAAGAGAGCCCGGTGTG 561
   ::::::::::::::::::::

QY 136 MetValAlaVal---TriIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSer 154
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Db 562 ATGATCGGTCTGGCTTGGTCATCTCTTTCCTTGGCTCCTGCCATCTTG----- 615
   ::::::::::::::::::::

QY 155 AspSerTrp-----LysAsnSerThrAsnThrGluGluCysGluProGly 169
   ::::::::::::::::::::
Db 616 ---TTCTGGCAATACTTTTGTGAAAGAGAACTGTGCTCTCGGAGAGTGTTCATTACAG 672
   ::::::::::::::::::::

QY 170 PheValThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProVal 189
   ::::::::::::::::::::
Db 673 TTCTCAGTGAGCCCAACCATTAATCTTTTGGCAGACCATCGTCTTTTATATGCTGTG 732
   ::::::::::::::::::::

QY 190 SerLeuValValTyrPheSerValGln----- 198
   ::::::::::::::::::::
Db 733 ACCATTATGAC-TATTTTATCTGGAGGATCTATAGGAACCTGAAAGCGTACCACAGA 791
   ::::::::::::::::::::

QY 199 IleTyrTrp-----SerLeuTrpLysArgGly---SerLeuSerArgCysProSerHis 215
   ::::::::::::::::::::
Db 792 GCTTGTGCGCTCGCAAGCCTCTGGGACAGAGCAGACAGAGAAACTTTGTCCACCCAC 851
   ::::::::::::::::::::

QY 216 AlaGlyPheIleAlaThrSerSerArgGlyThrGly----- 227
   ::::::::::::::::::::
Db 852 GGGCAGTTTCTCGAAGCTGCAGCAGTTTACGAACCTTCAACAGCAAGCATGAACGCTCAA 911
   ::::::::::::::::::::

QY 228 -----HisSerArgArgThrGlyLeuAlaCys 236
   ::::::::::::::::::::
Db 912 CAGGAGGAAGTATGGCGCTGCCACTTCTGGTTTCACCAAGCTGGAACCCAGCTC 971
   ::::::::::::::::::::

QY 237 ArgThrSer----- 239
   ::::::::::::::::::::
Db 972 CGAGCAGATGGACCAAGACCACAGCAGCAGTGACAGTTGGAAACAATGATGCTGCTGC 1031
   ::::::::::::::::::::

QY 240 LeuProGly-----LeuLysGluProAlaAla 248
   ::::::::::::::::::::
Db 1032 CTCCTTGGAGAACTCCGCTCTCCGACGAGGAGGACATTTGGCTCGACGAGAGGCCAT 1091
   ::::::::::::::::::::

QY 249 SerLeuHisSerGluSerProArgGlyLys-SerSerLeuLeuValSerLeuArgThrHi 268
   ::::::::::::::::::::
Db 1092 CTACTCCATCGTGTCAAGCTTCGGGTCACAGCACCATCTCACTCCACCAAGTTACC 1151
   ::::::::::::::::::::

QY 268 sMetSerGlySerIle-----I 274
   ::::::::::::::::::::
Db 1152 CTCATCGGACAACCTGCAGGTGCTCAGGAGGAGCTGGGATGGTGGACTTGGAGAGGAA 1211
   ::::::::::::::::::::

QY 274 eAlaPheLysVal-----GlySerPheCysArgSer-- 284
   ::::::::::::::::::::
Db 1212 AGCCGACAAGCTGCAGGCCCCAGAAAGCGTGGACGATGGAGGCGAGTTTTCACAAAGATT 1271
   ::::::::::::::::::::

QY 285 -----GluSerProVal----- 288
   ::::::::::::::::::::
Db 1272 CTCCAAGCTTCCATCCAGTACAGTACGCCGTGGACACAGCTTAAGACTTTCAGCTCAA 1331
   ::::::::::::::::::::

QY 288 ----- 288
   ::::::::::::::::::::
Db 1332 CTCCTCAGTGGGTAAAGACGACGCGCACTCTACCTCTGCTCTTCAAGGAAGCCACTCTGGC 1391
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QY 289 -----LeuHisGlnArgGluHisValGluLeuLe 298
   ::::::::::::::::::::
Db 1392 CAAGAGGTTTGTCTCTGAAGACCAAGAGTCAGATCACTAAACGCGAAAGGATGTCCCTGTG 1451
   ::::::::::::::::::::

QY 298 uArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTr 318
   ::::::::::::::::::::
Db 1452 CAAGGAGAAAGAACGCGCCAGACCTCAGTGGCGATCTTGTTCCTTCATCATCACTTG 1511
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QY 318 pAlaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLy 338
   ::::::::::::::::::::
Db 1512 GACCCCATACAACATCATGGTTCTGGTG---AACACCTTTTGTGACAGCTGCATACCCAA 1568
   ::::::::::::::::::::

QY 338 sSerIleTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPh 358
   ::::::::::::::::::::
Db 1569 AACCTTTTGG---AATCTGGGCTACTGGCTGTGTACATCAACAGCACCCTGAACCCCGT 1625
   ::::::::::::::::::::

QY 358 eLeuTyrProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeu-Cys---- 376
   ::::::::::::::::::::
Db 1626 GTGCTATGCTGTGTCACAAACAAACATTCAGAACCACTTTTCAAGATGCTCTGCTGTGCCA 1685
   ::::::::::::::::::::

QY 377 --ValThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391
   ::::::::::::::::::::
Db 1686 GTGTGACAAAAAAGAGCGCAAGCAGCAGTACCAGCAGACAGT 1732
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RESULT 6
LOCUS CB556920 672 bp mRNA linear EST 02-APR-2003
DEFINITION AMGNNUC:URGP1-00001-D6-A urgp1 (14349) Rattus norvegicus cDNA clone
urgp1-00001-d6 5', mRNA sequence.
ACCESSION CB556920
VERSION CB556920.1 GI:29496320
KEYWORDS EST.
SOURCE Rattus norvegicus (Norway rat)
ORGANISM Rattus norvegicus
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
Rattus.
REFERENCE 1 (bases 1 to 672)
AUTHORS Amgen EST Program.
TITLE Amgen Rat EST Program
JOURNAL Unpublished (2003)
COMMENT Contact: Dan Fitzpatrick
Amgen, Inc
One Amgen Center Drive, Thousand Oaks, CA 91320-1799, USA
Tel: 805 447-4881
Plate: 00001 row: d column: 6.
FEATURES
source
1..672
/organism="Rattus norvegicus"
/mol_type="mRNA"
/db_xref="taxon:10116"
/clone="urgp1-00001-d6"
/clone_lib="urgp1 (14349)"
/note="Vector: pSPORT1; Rat GPCR library rearranged
internal pSPORT vector"
ORIGIN
Alignment Scores:
Pred. No.: 5,93e-29 Length: 672
Score: 401.00 Matches: 80
Percent Similarity: 71.83% Conservative: 22
Best Local Similarity: 56.34% Mismatches: 36
Query Match: 19.61% Indels: 4
DB: 6 Gaps: 2
US-10-626-126-9 (1-391) x CB556920 (1-672)
QY 18 LeuAlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyAsnAlaValIle 37
   ::::::::::::::::::::
Db 227 CTGGCTGCGCTCATGCGCTGCTCATCGTGGCCACAGTACTGGGCAACGCGTGTGTCATG 286
   ::::::::::::::::::::

QY 38 LeuAlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeu 57
   ::::::::::::::::::::
Db 287 CTCGCTTCGTGGCGATTTCGAGCTCCGCCACCCAGAACAACTTCTTCTGCTCAACCTC 346
   ::::::::::::::::::::

QY 58 AlaIleSerAspPhePheValGlyValIleSerIleProLeuTyrIleProHisThrLeu 77
   ::::::::::::::::::::
Db 347 GCCATCTCCGACTCTCTCGTGGGTGCTCTTCATCCCATCTTGTACGTACCTATGTGTG 406
   ::::::::::::::::::::

QY 78 Phe---AsnTrpAsnProGlySerGlyIleCysMetPheTrpLeuIleThrAspTyrLeu 96
   ::::::::::::::::::::
```



## ORIGIN

## Alignment Scores:

Pred. No.: 6,39e-28 Length: 1770  
 Score: 397,50 Matches: 136  
 Percent Similarity: 41,31% Conservative: 85  
 Best Local Similarity: 25,42% Mismatches: 160  
 Query Match: 19,44% Indels: 155  
 DB: 9 Gaps: 18

US-10-626-126-9 (1-391) x AY400784 (1-1770)

QY 4 SerAsnGlyThrAspValLeuProLeuThrAlaGln-----ValProLeu 18  
 DB 151 TCAATGACACCTCCAGTGAACCTCTAGGGGGCCACACCATCTGGCAAGTGGTCTTCATT 210  
 QY 19 AlaPheLeuMetSerLeuLeuAlaPheAlaIleThrIleGlyValAlaValValLeu 38  
 DB 211 GCATTCTTGACTGGCTTCTGGCATTTGGTGACCATCATCGGCAACATCTTGTTCATTGTG 270  
 QY 39 AlaPheValAlaAspArgAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAla 58  
 DB 271 GCATTTAAGTCAACAACAGCTGAAGACAGTCAACAACATCTCTCTTTAAGCCTGGCC 330  
 QY 59 IleSerAspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe 78  
 DB 331 TGGCGAGATCTGATCATCTCGGGGTCAITTTCCATGAACCTGTTACGACCTACATCATATG 390  
 QY 79 Asn---TrpAsnProGlySerGlyIleCysMetPheTrpIleThrAspTyrLeuLeu 97  
 DB 391 AACCGCTGGGCTCTGGGAACTTAGCCTGTGACCTCTGGCTTTCCATTGATGATGTGGCC 450  
 QY 98 CysThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSer 117  
 DB 451 AGCAATGCTCTCTCATGATCTGCTGGTGCATCAGCTTTGACAGTACTTTCTTATATACC 510  
 QY 118 AsnAlaValArgTyrArgAlaGlnHisThrGlyIleLeuLysIleValAlaGlnMetVal 137  
 DB 511 AGGCCACTCACTTACCGAGCAACGAACA-----ACAAACGAGCGGTGTGATGATT 564  
 QY 138 AlaVal---TrpIleLeuAlaPheLeuValAsnGlyProMetIleLeuAlaSerAspSer 156  
 DB 565 GGTCTGGCTTGGTGCATCTCTTGTCTGTGGCTCTCTGCCATCTTG-----TTC 615  
 QY 157 Trp-----LysAsnSerThrAsnThrGluGluCysGluProGlyPheVal 171  
 DB 616 TGCAATACTTTGTAGGAAGAACTGTGCCCCCGGAGAAATGTTTCATTCACTTCTTA 675  
 QY 172 ThrGluTrpTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuProValSerLeu 191  
 DB 676 AGTGAGCCCACTACCTACCTTGGCAGCGGATCGCTGCTTTTACATGCTGTGCACCATC 735  
 QY 192 ValValTyrPheSerValGln-----IleTyr 200  
 DB 736 ATGAC-TATTTTATCTGGAGAACTTATAAGGAGACTGAGAAACGTACCAAGAGCTGGC 794  
 QY 201 TrpSer-----LeuTrpLysArg---GlySerLeuSerArgCysProSerHisAlaGly 217  
 DB 795 TGGGCTACAGGCTCTGGGACAGAGCGGAGAGAGAAACTTGTCCACCCCAAGCAG 854  
 QY 218 PheIle-----AlaThrSerSerArg-GlyThrGlyHisSerArgAr 231  
 DB 855 TTCTCGAAGCTGTAGCAGCTATGAGCTTACAACAGCAGGACGAAACGGTCACTAGGAG 914  
 QY 231 gThrGlyLeuAlaCys-----ArgThrSerLeuProGlyLeuLys-- 244  
 DB 915 GAAGATATGGTGGTGTCACTTCTGTTTCAACAACATAAGAGCTGGAAGCCAGTGTGAGCA 974  
 QY 245 -----GluProAlaIleSerLe 250  
 DB 975 GATGGACCAAGACACAGTAGCAGTGCAGTTGGATTAACAACAGATGCTGCTGCTCCCT 1034  
 QY 250 uHisSerGluSerProArg----- 256

DB 1035 GGAATACTCTGCTTCTTCTGATGAAGAGGATATTGGCTCAGACAGCAGCCATCTATTTC 1094  
 QY 257 -----GlyLysSerSerLeuLeuValSerLeuArgThrHisMetSe 270  
 DB 1095 CATTGTACTCAAGCTCGCGGTCATAGCAGCATCTCAACTCTTACCAAGTACCTCTCCTC 1154  
 QY 270 rGlySerIle----- 273  
 DB 1155 AGATAACCTGCAGGTGCCAGACAAGGACCTGGGGACTATGGATGTAGAGAGAAATGCCCA 1214  
 QY 273 ----- 273  
 DB 1215 TAAGCTTCAGGCCCAAGAGAGTATGATGACCGTGCAACTGTGCAAGAGGACTTCTCAA 1274  
 QY 273 ----- 273  
 DB 1275 GCTCCCATCCAGTTAGAGTCTGCCGTGGACACAGCCAGACCTCTGACACCAACTCCTC 1334  
 QY 274 -----TleAlaPheLysValGlySer----- 280  
 DB 1335 GGTGGACAAGACCCAGCGCGCTCTACCTCTGTCTTCAAGAAGCCACGCTGGCTAAGAG 1394  
 QY 281 -PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgG 300  
 DB 1395 GTTGTCTCTCAAGACCAAGTCAAGATCAACCAAGCGGAAAGGATGTGCTCATCAAGGA 1454  
 QY 300 YATGlyLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPr 320  
 DB 1455 GAAAGAGCGGCCCAACACACTAGTCCATCTTGTGGCTTTTATCATCATCAGTGGACCCC 1514  
 QY 320 oTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIl 340  
 DB 1515 CTACAACATCATGTGCTCTGTG---AACACCTTCTGTGACAGCTGCATACCCAAAACCTA 1571  
 QY 340 eTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTy 360  
 DB 1572 TTGG---AATCTGGGTACTGGCTGTGTATATCAACAGCACCGTGAACCCCGTGTGCTA 1628  
 QY 360 rProLeuCysHisArgArgPheGlnLysAlaPheTrpLysIleLeu-----CysVa 377  
 DB 1629 TGCCCTGTGCAACACAGACATTCAGAACCCACTTCAAGATGCTTCTTATGCCAGTGTGA 1688  
 QY 377 lThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391  
 DB 1689 CAAGAGGAGCGCGCAACACAGCAGTACCAGCAGACAGCAGTCC 1731

## RESULT 9

AK080950

LOCUS

DEFINITION

ACCESSION

VERSION

KEYWORDS

SOURCE

ORGANISM

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

PUBMED

REFERENCE

AUTHORS

TITLE

JOURNAL

MEDLINE

AK080950 3171 bp mRNA linear HTC 03-APR-2004  
 Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length  
 enriched library, clone:B430217G05 product:MUSCARINIC ACETYLCHOLINE  
 RECEPTOR M3 (MM3, MACHR), full insert sequence.

AK080950.1 GI:26348896

HTC; CAP trapper.

Mus musculus (house mouse)

Mus musculus

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;

Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.

1

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

High-efficiency full-length cDNA cloning

Meth. Enzymol. 303, 19-44 (1999)

99279253

10349636

2

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K.,

Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.

Normalization and subtraction of cap-trapper-selected cDNAs to

prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

20499374



Db 1579 TGGGCTACAGGCTCTGGGACAGCGGAAGCAGAAAACTTTGTCCACCCACAGGCAG 1638  
Qy 218 Pheile-----AlaThrSerSerArg-GlyThrGlyHisSerArgAr 231  
Db 1639 TTCTCGAAGCTGTAGCAGCTATGAGCTACACAGCAAGGCACAAACGGTCACTTAGGAG 1698  
Qy 231 gThrGlyLeuAlaCys-----ArgThrSerLeuProGlyLeuLys-- 244  
Db 1699 GAAGTATGGTGGTGTCTCACTTCTGTTTCAACAATGAAGCTGGAAGCCAGTCTGCAGCA 1758  
Qy 245 -----GluProAlaAlaSerLe 250  
Db 1759 GATGGACCAAGACCACAGTAGCAGTGACAGTTGGAATAACAACGATGCTGCTCCCTCCCT 1818  
Qy 250 uHisSerGluSerProArg----- 256  
Db 1819 GGAANAACCTGCTCTTCTGATGAAGAGGATATGGCTCAGAGACCAGACCATCTATTTC 1878  
Qy 257 -----GlyLysSerSerLeuLeuValSerLeuArgThrHisMetSe 270  
Db 1879 CATTTGACTCAAGCTGCGGGTCTATGACCATCTCTCAACTTACCAGCTACCCCTCCTC 1938  
Qy 270 rGlySerIle----- 273  
Db 1939 AGATAACCTGACAGTCCAGCAAGACCTGGGAGTATGGATGTAGAGAGAAATGCCCA 1998  
Qy 273 ----- 273  
Db 1999 TAAGTCTCAGGCCAGAGAGTATGGATGACCGTGACACTGTTCAGAGGACTTCTCCAA 2058  
Qy 273 ----- 273  
Db 2059 GCTCCCCATCCAGTTAGAGTCTGCGTGGACACAGCCAGACCTCTGACACCAACTCCTC 2118  
Qy 274 -----lleAlaPheLysValGlySer----- 280  
Db 2119 GTTGGACAAGACCGCGCTCTACTCTGCTCTTCAAAGAAGCCAGCCGCTGGCTAAGAG 2178  
Qy 281 -PheCysArgSerGluSerProValLeuHisGlnArgGluHisValGluLeuLeuArgG1 300  
Db 2179 GTTGTCTCAGACCAAGAGTACAGTACCAGCGGAAAGAGTGTGCTCATCAGGA 2238  
Qy 300 yArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAlaIleCysTrpAlaPr 320  
Db 2239 GAAGAAGCGCGCCAGACACTCAGTGCCTTTGCTGGCTTTTCATCATCAGCTGGACCCC 2298  
Qy 320 oTyrCysLeuPheThrIleValLeuSerThrTyrArgArgGlyGluArgProLysSerIl 340  
Db 2299 CTACAACATCATGCTCCTGGTG---AACACCTTCTGTGACAGCTGCATACCCAAAACCTA 2355  
Qy 340 eTTrpTyrSerIleAlaPheTrpLeuGlnTrpPheAsnSerLeuIleAsnProPheLeuTy 360  
Db 2356 TTGG---ANTCTGGGTACTGGCTGTGCTATATCAACAGACCGTGAACCCCTGTGCTA 2412  
Qy 360 rProLeuCysHisArgPheGlnLysAlaPheTrpLysIleLeu-----CysVa 377  
Db 2413 TGCCCTGTGCAACAAGACATTCAGAACCCACCTTCAAGATGCTTCTTATGCCAGTGTGA 2472  
Qy 377 lThrLysGlnProAlaProSerGlnThrGlnSerValSerSer 391  
Db 2473 CAAGAGGAAGCGCGCAACAGCAGTACCAAGCAGACAGTCC 2515

RESULT 10  
LOCUS AK032763  
DEFINITION Mus musculus 12 days embryo male wolffian duct includes surrounding region cDNA, RIKEN full-length enriched library, clone:6720430L06  
product:HISTAMINE RECEPTOR H1, full insert sequence.  
ACCESSION AK032763  
VERSION AK032763.1 GI:26328544  
KEYWORDS HTC; CAP trapper.  
SOURCE Mus musculus (house mouse)

ORGANISM Mus musculus  
REFERENCE 1  
AUTHORS Carninci, P. and Hayashizaki, Y.  
TITLE High-efficiency full-length cDNA cloning  
JOURNAL Meth. Enzymol. 305, 19-44 (1999)  
MEDLINE 99279253  
PUBMED 10349636  
REFERENCE 2  
AUTHORS Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
TITLE Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes  
JOURNAL Genome Res. 10 (10), 1617-1630 (2000)  
MEDLINE 20499374  
PUBMED 11042159  
REFERENCE 3  
AUTHORS Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsumai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hazada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwaki, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Oneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
TITLE RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer  
JOURNAL Genome Res. 10 (11), 1757-1771 (2000)  
MEDLINE 20530913  
PUBMED 11076861  
REFERENCE 4  
AUTHORS The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
TITLE Functional annotation of a full-length mouse cDNA collection  
JOURNAL Nature 409, 685-690 (2001)  
REFERENCE 5  
AUTHORS The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
TITLE Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
JOURNAL Nature 420, 563-573 (2002)  
REFERENCE 6  
AUTHORS Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
TITLE Direct Submission  
SUBMITTED (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsc.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)  
COMMENT cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in Riken. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/  
Location/Qualifiers  
1. .2780  
/organism="Mus musculus"

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/note="unnamed protein product; HISTAMINE RECEPTOR H1
(SPTR|Q91V75, evidence: FASTV, 100%ID, 100%length,
match=1464)
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QSLSTRISQYVSGHLNRRKAAKGLCIMAFLCWPYPIFFWVIAFCNSCCSEPV
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```

CDS

## ORIGIN

## Alignment Scores:

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Pred. No.:      4,18e-27      Length:      2780
Score:          392.50        Matches:     126
Percent Similarity: 42.74%    Conservative: 80
Best Local Similarity: 26.14%  Mismatches:    159
Query Match:      3          Indels:       118
DB:               3          Gaps:        18

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US-10-626-126-9 (1-391) x AK032763 (1-2780)

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QY 1 MetSerGluSerAsnGlyThrAspValLeuProLeuThrAlaGlnValProLeuAlaPhe 20
DB 109 ATGTGTGAGGGGAACAGGACA---GCCATGGCCAGCCCTCAGCTGTCGCCCTGGTGGTG 165
QY 21 LeuMetSerLeuLeuAlaPheAlaIleThrIleGly---AsnAlaValValIleLeuAla 39
DB 166 GTTCTAAGTAGTATCTCCCTG---GTCACAGTGGGGCCTCAACCTGCTGGTGTGTATGCA 222
QY 40 PheValAlaAspAsnLeuArgHisArgSerAsnTyrPhePheLeuAsnLeuAlaIle 59
DB 223 GTGCGCAGTGAGGCGCAAGCTACACACCGTGGGCAACCTGTATGTCAGCCTGTCGGTA 282
QY 60 SerAspPheValGlyValIleSerIleProLeuTyrIleProHisThrLeuPhe--- 78
DB 283 GCAGACCTGATTGTAGGGCAGCTGCTGATGCCCATGAACATCTCTATCTTATCATGACC 342
QY 79 AsnTyrAsnProGlySerGlyIleCysMetPheTyrLeuIleThrAspTyrLeuLeuCys 98
DB 343 AAGTGGTCCCTGGCGCGCCCTCTGCTCTTTGGCTCTCTATGATTATGTGGCCAGC 402
QY 99 ThrAlaSerValTyrSerIleValLeuIleSerTyrAspArgTyrGlnSerValSerAsn 118
DB 403 ACGGCATCCATCTTATGTCTTCATCTGCTGTTGATTGATCGCTACCGCTCTGTCCAGCAA 462
QY 119 AlaValArgTyrArgAlaGlnHisThrGlyIleLeuLeuIleValAlaGlnMetValAla 138
DB 463 CCCTCCGGTACTGAGGTATCGAACCAG---ACCGTGCTTCAGCTACCATCTCTGGGG 519
QY 139 ValTyrIleLeuAlaPheLeuValaAnGlyProMetIleLeuAlaSerAspSerTyrPlys 158
DB 520 GCCTGGTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCTCT 567
QY 159 AsnSerThr-----AenThrGluGluCysGluProGlyPheValThr 172
DB 568 CACTTCACGCCCTCGCCCCAGAGCTTCGGGAAGATAAGTGTGAGACAGATTCTACAAAT 627

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QY 173 GluTyrTyrIleLeuAlaIleThrAlaPheLeuGluPheLeuLeuProValSerLeuVal 192
DB 628 GTCACTTGGTTCAAGATCATGACCGCCATCATCAACTTCTACCTCCCCCACTTTGCTCATG 687
QY 193 ValTyrPheSerValGlnIleTyr----- 200
DB 688 CTGTGGTTCTATGTGAAGATCTACAGGCTGTGGGGCAGACTGTCAACACCGCCAGCTC 747
QY 200 ----- 200
DB 748 ACCAACGGGTCCCTCCCTACCTTTTAGAAATCAAGCTGAGTCCGAGGATGCCAAAGAG 807
QY 201 -----TyrSerLeuTyrPheArg----- 206
DB 808 GGTGCCAAAGAACCTGGGAAAGAGTCTCCCTGGGGGTCAGAGAGAGCGCTCAAGAGAC 867
QY 207 -----GlySerLeuSerArgCysProSerHisAlaGly-PheIle 219
DB 868 CCTACTGGAGGTCTGGATCAGAGTCAACATCTGAAGACCCCAAGGTGACCTCTCGACT 927
QY 219 eAlaThrSerSerArgGlyThrGlyHisSerArgArgThrGlyLeu-----Al 235
DB 928 GTCTTCAGCAAGAGGGGGGAAAGAGTCAACACGCCCTGTTCGTCTTGACGTC 987
QY 235 aCysArgThrSerLeu-----ProGlyLeuLysGluProAlaAlaSerLe 250
DB 988 ATGCAGACACAGCCTGTCCTGAGGAGATGCCAGGGGCTCAAGGCCAAATGAC-CAGAC 1046
QY 250 uHisSerGluSerProArgGlyLysSerSerLeu----- 261
DB 1047 CTTGAGCCAGCCCAAAATGGATGAGCAGAGCTGAGTACTTCCCGCGGATCAGTGAGAC 1106
QY 262 -----LeuValSer-----LeuArgThrHisMetSerGlySe 272
DB 1107 ATCAGAGGACACAGACCTTGGTGGATCGACAGTCTCTCCCGGACCACAGACTCAGACAC 1166
QY 272 rIleIle-----AlaPheLysValGlySerPheCysArgSerGluSerProVal-- 288
DB 1167 CAGCATAGACGAGCGGTGGGCAAGTCAAGCGAGAGAGAGGTCTAAGTGGCGTGA 1226
QY 289 -----LeuHisGlnArgGluHisVal----- 295
DB 1227 CTACATCAAGTCACTCGAAGAGGCTCGCTCACAATCCAGACAGATGTGTCCGGGT 1286
QY 296 -GluLeuLeuArgGlyArgLysLeuAlaArgSerLeuAlaValLeuLeuSerAlaPheAl 315
DB 1287 GCACCTTGAACCGAGAGCGAAGGAGCAAGCAGTGTGGTGTGTATCATGCGCAGCATTCAT 1346
QY 315 aIleCysThrPalaProTyrCysLeuPheThrIleValLeuSerThrTyrArgArg--G 334
DB 1347 TCTCTGCTGGATTCCCTATTTCATCTTCTATGTCATTCCTCTCTGTCGCAACAGCTGTG 1406
QY 334 yGluArgProLysSerIleTyrTyrSerIleAlaPheTyrLeuGlnTyrPheAsnSerLe 354
DB 1407 CAGCGAACCTGTG-----CACATGTCACCATTTGGCTGGGCTACATCACTCCAC 1457
QY 354 uIleAsnProPheLeuTyrProLeuCysHisArgArgPheGlnLysAlaPheTyrPlysIl 374
DB 1458 GCTGAACCCCTCATCTACCTGTCGCAACGAGAACTTCAAGAGAGACATTCAAAAAAAT 1517
QY 374 eLeu 375
DB 1518 TCTG 1521

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## RESULT 11

AK047070

LOCUS

DEFINITION

Mus musculus 10 days neonate cerebellum cDNA, RIKEN full-length  
enriched library, clone:B930016C09 product:HISTAMINE RECEPTOR HL,  
full insert sequence.

ACCESSION

AK047070

VERSION

AK047070.1 GI:26338557

AK047070 2831 bp mRNA linear HTC 03-APR-2004

## KEYWORDS

SOURCE Mus musculus (house mouse)  
ORGANISM Mus musculus

## REFERENCE

AUTHORS Carninci, P. and Hayashizaki, Y.

TITLE High-efficiency full-length cDNA cloning

JOURNAL Meth. Enzymol. 303, 19-44 (1999)

MEDLINE 99279253

PUBMED 10349636

## REFERENCE

AUTHORS

Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes

Genome Res. 10 (10), 1617-1630 (2000)

JOURNAL 20499374

MEDLINE 11042159

## REFERENCE

AUTHORS

Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Hara, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsuura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
RIKEN integrated sequence analysis (RISA) system--384-format sequencing pipeline with 384 multicapillary sequencer

Genome Res. 10 (11), 1757-1771 (2000)

JOURNAL 20530913

MEDLINE 11076861

## REFERENCE

AUTHORS

The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.

Functional annotation of a full-length mouse cDNA collection

Nature 409, 695-690 (2001)

## REFERENCE

AUTHORS

The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.

Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs

Nature 420, 563-573 (2002)

## REFERENCE

AUTHORS

Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Inotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Kato, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koya, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, I., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct Submission

Submitted (16-JUL-2001)

Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute; 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gsr.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

cDNA library was prepared and sequenced in Mouse Genome

Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.

Please visit our web site for further details.

URL: http://genome.gsc.riken.jp/

URL: http://fantom.gsc.riken.jp/

Location/Qualifiers

## FEATURES

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Query Match: 19.19% Indels: 118  
DB: 3 Gaps: 18

## ORIGIN

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## RESULT 12

AK038480

LOCUS

DEFINITION Mus musculus adult male hypothalamus cDNA, RIKEN full-length enriched library, clone:A230019E03 product:HISTAMINE RECEPTOR H1, full insert sequence.

ACCESSION

AK038480

VERSION  
KEYWORDS  
SOURCE  
ORGANISMAK038480.1 GI:26332590  
HTC, CAP trapper.  
Mus musculus (house mouse)  
Mus musculusREFERENCE  
AUTHORS  
TITLE  
JOURNAL  
MEDLINE  
PUBMED1  
Carninci, P. and Hayashizaki, Y.  
High-efficiency full-length cDNA cloning  
Meth. Enzymol. 303, 19-44 (1999)  
99279253  
10349636REFERENCE  
AUTHORS2  
Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.  
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20499374  
11042159REFERENCE  
AUTHORS3  
Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsuai, T., Tashiro, H., Itoh, M., Sumi, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Ishikawa, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.  
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20530913  
11076861REFERENCE  
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The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.  
Functional annotation of a full-length mouse cDNA collection  
Nature 409, 685-690 (2001)REFERENCE  
AUTHORS5  
The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.  
Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs  
Nature 420, 563-573 (2002)REFERENCE  
AUTHORS6  
(bases 1 to 2979)  
Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, S., Konno, H., Kouda, M., Koye, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Hayashida, K., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.  
Direct SubmisionREFERENCE  
AUTHORS

Submitted (16-JUN-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@gs.riken.jp, URL: http://genome.gsc.riken.jp/, Tel: 81-45-503-9222, Fax: 81-45-503-9216)

## COMMENT

cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues.  
Please visit our web site for further details.  
URL: http://genome.gsc.riken.jp/  
URL: http://fantom.gsc.riken.jp/.



FEATURES  
source

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## CDS

Alignment Scores:  
Pred. No.: 4,67e-27 Length: 2979  
Score: 392.50 Matches: 126  
Percent Similarity: 42.74% Conservative: 80  
Best Local Similarity: 26.14% Mismatches: 159  
Query Match: 19.19% Indels: 118  
DB: 3 Gaps: 18

## ORIGIN

US-10-626-126-9 (1-391) x AK038480 (1-2979)  
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AK046607  
LOCUS  
DEFINITION  
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Mus musculus 4 days neonate male adipose cDNA, RIKEN full-length  
enriched library, clone:B430204G09 product:HISTAMINE RECEPTOR H1,

ACCESSION	AK046607	full insert sequence.	URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a>
VERSION	AK046607.1	GI:26338238	URL: <a href="http://fantom.gsc.riken.jp/">http://fantom.gsc.riken.jp/</a>
KEYWORDS	HTC; CAP trapper.		
SOURCE	Mus musculus (house mouse)		Location/Qualifiers
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AUTHORS	Carninci, P. and Hayashizaki, Y.		/mol_type="mRNA"
TITLE	High-efficiency full-length cDNA cloning		/strain="C57BL/6J"
JOURNAL	Meth. Enzymol. 303, 19-44 (1999)		/db_xref="PANTOM.DB:B430204G09"
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AUTHORS	Carninci, P., Shibata, Y., Hayatsu, N., Sugahara, Y., Shibata, K., Itoh, M., Konno, H., Okazaki, Y., Muramatsu, M. and Hayashizaki, Y.		/tissue_type="adipose"
TITLE	Normalization and subtraction of cap-trapper-selected cDNAs to prepare full-length cDNA libraries for rapid discovery of new genes		/clone_lib="RIKEN full-length enriched mouse cDNA library"
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AUTHORS	Shibata, K., Itoh, M., Aizawa, K., Nagaoka, S., Sasaki, N., Carninci, P., Konno, H., Akiyama, J., Nishi, K., Kitsunai, T., Tashiro, H., Itoh, M., Suni, N., Ishii, Y., Nakamura, S., Hazama, M., Nishine, T., Harada, A., Yamamoto, R., Matsumoto, H., Sakaguchi, S., Ikegami, T., Kashiwagi, K., Fujiwara, S., Inoue, K., Togawa, Y., Izawa, M., Ohara, E., Watahiki, M., Yoneda, Y., Iihiki, T., Ozawa, K., Tanaka, T., Matsura, S., Kawai, J., Okazaki, Y., Muramatsu, M., Inoue, Y., Kira, A. and Hayashizaki, Y.		/codon_start=1
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JOURNAL	Genome Res. 10 (11), 1757-1771 (2000)		/db_xref="GI:26338239"
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REFERENCE	4		Alignment Scores:
AUTHORS	The RIKEN Genome Exploration Research Group Phase II Team and the FANTOM Consortium.		Pred. No.: 6,9e-27
TITLE	Functional annotation of a full-length mouse cDNA collection		Score: 392.50
JOURNAL	Nature 409, 695-699 (2001)		Length: 3783
REFERENCE	5		Matches: 126
AUTHORS	The FANTOM Consortium and the RIKEN Genome Exploration Research Group Phase I & II Team.		Percent Similarity: 42.74%
TITLE	Analysis of the mouse transcriptome based on functional annotation of 60,770 full-length cDNAs		Conservative: 80
JOURNAL	Nature 420, 563-573 (2002)		Best Local Similarity: 26.14%
REFERENCE	6 (bases 1 to 3783)		Mismatches: 159
AUTHORS	Adachi, J., Aizawa, K., Akimura, T., Arakawa, T., Bono, H., Carninci, P., Fukuda, S., Furuno, M., Hanagaki, T., Hara, A., Hashizume, W., Hayashida, K., Hayatsu, N., Hiramoto, K., Hiraoka, T., Hirozane, T., Hori, F., Imotani, K., Ishii, Y., Itoh, M., Kagawa, I., Kasukawa, T., Katoh, H., Kawai, J., Kojima, Y., Kondo, H., Kouda, M., Koyas, S., Kurihara, C., Matsuyama, T., Miyazaki, A., Murata, M., Nakamura, M., Nishi, K., Nomura, K., Numazaki, R., Ohno, M., Ohsato, N., Okazaki, Y., Saito, R., Saitoh, H., Sakai, C., Sakai, K., Sakazume, N., Sano, H., Sasaki, D., Shibata, K., Shinagawa, A., Shiraki, T., Sogabe, Y., Tagami, M., Tagawa, A., Takahashi, F., Takaku-Akahira, S., Takeda, Y., Tanaka, T., Tomaru, A., Toya, T., Yasunishi, A., Muramatsu, M. and Hayashizaki, Y.		Query Match: 19.19%
TITLE	Direct Submission		Indels: 118
JOURNAL	Submitted (16-JUL-2001) Yoshihide Hayashizaki, The Institute of Physical and Chemical Research (RIKEN), Laboratory for Genome Exploration and Research Group, RIKEN Genomic Sciences Center (GSC), RIKEN Yokohama Institute, 1-7-22 Suehiro-cho, Tsurumi-ku, Yokohama, Kanagawa 230-0045, Japan (E-mail: genome-res@sc.riken.jp, URL: <a href="http://genome.gsc.riken.jp/">http://genome.gsc.riken.jp/</a> , Tel: 81-45-503-9222, Fax: 81-45-503-9216)		Gaps: 18
REFERENCE	cDNA library was prepared and sequenced in Mouse Genome Encyclopedia Project of Genome Exploration Research Group in Riken Genomic Sciences Center and Genome Science Laboratory in RIKEN. Division of Experimental Animal Research in Riken contributed to prepare mouse tissues. Please visit our web site for further details.		US-10-626-126-9 (1-391) x AK046607 (1-3783)
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VERSION
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Clark, A.G., Glanowski, S., Nielson, R., Thomas, P., Kejariwal, A.,
Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,
Adams, M.D. and Cargill, M.
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,
Rockville, MD 20850, USA
This sequence was made by sequencing genomic exons and ordering
them based on alignment.
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Percent Similarity: 27.85% Mismatches: 159
Best Local Similarity: 18.95% Indels: 43
Query Match: 9 Gaps: 11
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US-10-626-126-9 (1-391) x AY415605 (1-1173)
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Todd, M.A., Tanenbaum, D.M., Civeello, D.R., Lu, F., Murphy, B.,  
Ferriera, S., Wang, G., Zheng, X.H., White, T.J., Sninsky, J.J.,  
Adams, M.D. and Cargill, M.  
Direct Submission  
Submitted (16-NOV-2003) Celera Genomics, 45 West Gude Drive,  
Rockville, MD 20850, USA  
This sequence was made by sequencing genomic exons and ordering  
them based on alignment.

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ORIGIN  
Alignment Scores: 3.2e-27 Length: 1173  
Pred. No.: 387.50 Matches: 105  
Score: 46.42% Conservative: 70  
Percent Similarity: 27.85% Mismatches: 159  
Best Local Similarity: 18.95% Indels: 43  
Query Match: 9 Gaps: 11  
DB: 11

US-10-626-126-9 (1-391) x AY415605 (1-1173)

Qy 8 AspValLeuProLeuThrAlaGlnValProLeuAlaPheLeuMetSerLeuLeuAlaPhe 27  
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Job time : 3195 secs

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GenCore version 5.1.6  
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: August 3, 2005, 01:37:47 ; Search time 170 Seconds

(without alignments)  
1177.782 Million cell updates/sec

Title: US-10-626-126-9

Perfect score: 2045

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Scoring table:

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Gapop 10.0 , Gapext 0.5

Searched: 1612378 seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%

Maximum Match 100%

Listing first 45 summaries

Database : UniProt 03.\*

1: uniprot\_sprot.\*

2: uniprot\_trembl.\*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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2	1742	85.2	391	2 Q912Y2	Q912y2 mus musculu
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6	1237.5	60.5	389	2 Q912Y3	Q912y3 cavia porce
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OC	Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.			
OX	NCBI_TaxID=10116;			
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RP	SEQUENCE FROM N.A.			
RC	STRAIN=Sprague-Dawley;			
RA	Liu C., Wilson S., Kuei C., Lovenberg T.W.;			
RL	Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.			
CC	-!- SURCELLULAR LOCATION: Integral membrane protein (By similarity).			
CC	-!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.			
DR	EMBL; AF358860; AAK97381.1; -			
DR	GO; GO:0016021; C:integral to membrane; IEA.			
DR	GO; GO:0004872; F:rhodopsin-like receptor activity; IEA.			
DR	GO; GO:0001584; F:rhodopsin coupled receptor protein signalin. .; IEA.			
DR	GO; GO:0007186; P:G-protein coupled receptor			
DR	Pfam; PF00001; 7tm 1; 1.			
DR	PRINTS; PR00237; GPCRHHODOPSN.			
DR	PRINTS; PR01726; HISTAMINEH4R.			
DR	PROSITE; PS00237; G PROTEIN RECP F1_1; 1.			
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Query Match 99.5%; Score 2034; DB 2; Length 391;				
Best Local Similarity 99.7%; Pred. No. 4 4e-142;				
Matches 390; Conservative 0; Mismatches 1; Indels 0; Gaps 0;				
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Db	181 AFLEFLLPVLVYVFSQIYWSLWKRGSLSRCSHAGFIATSRGTGHSRRTGLACRTSL 240			
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DT 01-OCT-2003 (TremBLrel. 25, Last annotation update)  
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GN Name=H4h4;  
OS Mus musculus (Mouse).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
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RP SEQUENCE FROM N.A.  
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RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF358859; AAK97380.1; -.  
DR MGD; MGI:2429635; Hrh4.  
DR GO; GO:0005615; C:extracellular space; TAS.  
DR GO; GO:0005887; C:integral to plasma membrane; IC.  
DR GO; GO:0005624; C:membrane fraction; IDA.  
DR GO; GO:0004969; F:histamine receptor activity; IDA.  
DR GO; GO:0006954; P:inflammatory response; TAS.  
DR Pfam; PF00001; 7cm1; 1.  
DR PRINTS; PR00237; GPCRHHODOPSN.  
DR PRINTS; PR01726; HISTAMINEH4.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 391 AA; 44248 MW; 59EC73CB5914C5E0 CRC64;

Query Match 85.2%; Score 1742; DB 2; Length 391;  
Best Local Similarity 84.9%; Pred. No. 1.6e-120;  
Matches 332; Conservative 17; Mismatches 42; Indels 0; Gaps 0;

Qy 1 MSESNGTDVLPETAQVPLAFLMSLLAFATIGNAVVILAFVADRLRHRSNYFFLNLAIS 60  
Db 1 MSESNGTILPPAAQVPLAFLMSFAFMVGNVAVILAFVVDRLRHRSNYFFLNLAIS 60  
Qy 61 DPFVGVISIPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYSLVSYDRYQSVSNV 120  
Db 61 DFLVGLIISIPLYIPHVLFWNFGSGICMFWLITDYLLCTASVYSLVSYDRYQSVSNV 120  
Qy 121 RYRAQHTGILKIVAQMVAVILAFVNGPMLASDSWKNSTNTECEPGFVTEWILAIT 180  
Db 121 SYRAQHTGIMKIVAQMVAVILAFVNGPMLASDSWKNSTNTECEPGFVTEWILAIT 180  
Qy 181 AFLEPFLPSLVVYFSVQIYNSLWKGSLRCPHAGFIATSSRGTSRRRTGLACRTSL 240  
Db 181 AFLEPFLPSLVVYFSVQIYNSLWKGSLRCPHAGFIATSSRGTSRRRTGLACRTSL 240  
Qy 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGSI IAFKVGSCFCSBSPVLHQREHVELLRG 300  
Db 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGSI IAFKVGSCFCSBSPVLHQREHVELLRG 300  
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGPRKSIWYSIAFWLQWPNLSINPFLY 360  
Db 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGPRKSIWYSIAFWLQWPNLSINPFLY 360

Qy 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391  
Db 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391

RESULT 3  
Q96LD9 PRELIMINARY; PRT; 390 AA.  
ID Q96LD9  
AC Q96LD9  
DT 01-DEC-2001 (TremBLrel. 19, Created)  
DT 01-DEC-2001 (TremBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TremBLrel. 24, Last annotation update)  
DE Histamine receptor H4.  
OS Homo sapiens (Human).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.  
OX NCBI\_TaxID=9606;  
RN [1]  
RP SEQUENCE FROM N.A.  
RX MEDLINE=21106319; PubMed=11179435;  
RA Nguyen T., Shapiro D.A., George S.R., Setola V., Lee D.K., Cheng R.,  
RA Rauser L., Lee S.P., Lynch K.R., Roth B.L., O'Dowd B.F.;  
RT "Discovery of a novel member of the histamine receptor family.";  
RL Mol. Pharmacol. 59:427-433(2001)  
CC -!- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -!- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AY008280; AAL09297.1; -.  
DR GO; GO:0016021; C:integral to membrane; IEA.  
DR GO; GO:0004872; F:receptor activity; IEA.  
DR GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO; GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.  
DR InterPro; IPR00276; GPCR\_Rhodopsn.  
DR InterPro; IPR008102; Histamine\_recept\_H4.  
DR Pfam; PF00001; 7cm1; 1.  
DR PRINTS; PR00237; GPCRHHODOPSN.  
DR PRINTS; PR01726; HISTAMINEH4.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 390 AA; 44469 MW; CC82B5D30D216C66 CRC64;

Query Match 68.7%; Score 1405.5; DB 2; Length 390;  
Best Local Similarity 69.1%; Pred. No. 1e-95;  
Matches 271; Conservative 41; Mismatches 77; Indels 3; Gaps 2;

Qy 1 MSESNGTDVLPETAQVPLAFLMSLLAFATIGNAVVILAFVADRLRHRSNYFFLNLAIS 60  
Db 1 MADTNTSINLSLSTRVTLAFMSLVAFALMLGNALVILAFVVDKLRHRSNYFFLNLAIS 60  
Qy 61 DPFVGVISIPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYSLVSYDRYQSVSNV 120  
Db 61 DPFVGVISIPLYIPHTLFNNPGSGICMFWLITDYLLCTASVYSLVSYDRYQSVSNV 120  
Qy 121 RYRAQHTGILKIVAQMVAVILAFVNGPMLASDSWKNSTNTECEPGFVTEWILAIT 180  
Db 121 SYRTQHTGVLKIVLAVVAVILAFVNGPMLVSVESWKEGSG--ECEPGFVTEWILAIT 178  
Qy 181 AFLEPFLPSLVVYFSVQIYNSLWKGSLRCPHAGFIATSSRGTSRRRTGLACRTSL 240  
Db 179 SPLEFVIFVILVAYFNMYNSLWKGSLRCPHAGFIATSSRGTSRRRTGLACRTSL 238  
Qy 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGSI IAFKVGSCFCSBSPVLHQREHVELLRG 300  
Db 239 SASTEVPAFHSERQRKSSLSLFFSSRTKNNSNTIASKMGSGFSQSDSVALHQREHVELLR 298  
Qy 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRRGPRKSIWYSIAFWLQWPNLSINPFLY 360  
Db 299 RKLARSLAIIILGVAVCAPYSLFTIVLSFVSSATGPKSVWYTRIAFWLQWPNLSINPFLY 358  
Qy 361 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 391  
Db 359 PLCHRRFOKAFWKILCVTKQAPSPQTSQSVSS 390



RESULT 4

HH4R HUMAN STANDARD; PRT; 390 AA.

AC Q9H3N8: Q9CZQ0; 16-OCT-2001 (Rel. 40, Created)

DT 16-OCT-2001 (Rel. 40, Last sequence update)

DT 25-OCT-2004 (Rel. 45, Last annotation update)

DE Histamine H4 receptor (HH4R) (GPRV53) (G protein-coupled receptor 105) (GPCR105) (SP9144) (AXOR35).

GN Name=HRH4;

OS Homo sapiens (Human).

OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

OX NCBI\_TaxID=9606;

RN [1]

RP SEQUENCE FROM N.A.

RX MEDLINE=20538417; PubMed=10973974; DOI=10.1074/jbc.M006480200;

RA Oda T., Morikawa N., Saito Y., Masuho Y., Matsumoto S.-I., Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; "Molecular cloning and characterization of a novel type of histamine receptor preferentially expressed in leukocytes."; J. Biol. Chem. 275:36781-36786(2000).

RN [2]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Leukocyte;

RX MEDLINE=20568725; PubMed=11118334; DOI=10.1006/bbrc.2000.4008;

RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.; "Molecular cloning and characterization of a new human histamine receptor, HH4R."; Biochem. Biophys. Res. Commun. 279:615-620(2000).

RN [3]

RP SEQUENCE FROM N.A.

RA Jones P.G., Wu S., Betty M.; "Cloning of a novel histamine receptor."; Submitted (SEP-2000) to the EMBL/GenBank/DBJ databases.

RN [4]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Bone marrow;

RX PubMed=11179434;

RA Liu C., Ma X.-J., Jiang X., Wilson S.J., Hofstra C.L., Blevitt J., Pyati J., Li X., Chai W., Carruthers N., Lovenberg T.W.; "Cloning and pharmacological characterization of a fourth histamine receptor (H4) expressed in bone marrow."; Mol. Pharmacol. 59:420-426(2001).

RN [5]

RP SEQUENCE FROM N.A., AND CHARACTERIZATION.

RC TISSUE=Eosinophil;

RX MEDLINE=21104636; PubMed=11181941;

RA Morse K.L., Behan J., Laz T.M., West R.E. Jr., Greenfeder S.A., Anthes J.C., Umland S., Wan Y., Hipkin R.W., Gonsiorek W., Shin N., Gustafson E.L., Qiao X., Wang S., Hedrick J.A., Greene J., Bayne M., Monsma F.J. Jr.; "Cloning and characterization of a novel human histamine receptor."; J. Pharmacol. Exp. Ther. 296:1058-1066(2001).

RN [6]

RP SEQUENCE FROM N.A.

RX MEDLINE=21106320; PubMed=11179436;

RA Zhu Y., Michalovich D., Wu H.-L., Tan K.B., Dytko G.M., Mannan I.J., Boyce R., Alston J., Tierney L.A., Li X., Herrity N.C., Vawter L., Sarau R.M., Ames R.S., Davenport C.M., Hieble P., Wilson S., Bergsma D.J., Fitzgerald L.R.; "Cloning, expression, and pharmacological characterization of a novel human histamine receptor."; Mol. Pharmacol. 59:434-441(2001).

RN [7]

RP SEQUENCE FROM N.A.

RA O'Reilly M.A.; "Identification of a histamine H4 receptor on human eosinophils - Role in eosinophil chemotaxis."; Submitted (JAN-2001) to the EMBL/GenBank/DBJ databases.

RN [8]

RP SEQUENCE FROM N.A.

RA Puhl H.I. III, Ikeda S.R., Aronstam R.S.; "cDNA clones of human proteins involved in signal transduction sequenced by the Guthrie cDNA resource center (www.cdna.org)."; Submitted (JUL-2002) to the EMBL/GenBank/DBJ databases.

CC -!- FUNCTION: The H4 subclass of histamine receptors could mediate the histamine signals in peripheral tissues. Displays a significant level of constitutive activity (spontaneous activity in the absence of agonist).

CC -!- SUBCELLULAR LOCATION: Integral membrane protein.

CC -!- TISSUE SPECIFICITY: Expressed primarily in the bone marrow and eosinophils. Shows preferential distribution in cells of immunological relevance such as T-cells, dendritic cells, monocytes, mast cells, neutrophils. Also expressed in a wide variety of peripheral tissues, including the heart, kidney, liver, lung, pancreas, skeletal muscle, prostate, small intestine, spleen, fetal liver and lymph node.

CC -!- INDUCTION: Expression is either up-regulated or down-regulated upon activation of the lymphoid tissues and this regulation may depend on the presence of IL-10 or IL-13.

CC -!- MISCELLANEOUS: Does not bind diphenhydramine, loratadine, ranitidine, cimetidine and chlorpheniramine. Shows modest affinity for dimaprit, imipromidine, clobenpropit, thioperamide, burinamide clobazepam, imipetit and imetit. The order of inhibitory activity was imetit > clobenpropit > burinamide > thioperamide. Clobenpropit behaves as a partial agonist, dimaprit and imipromidine show some agonist activity while clobazepam behaves as a full agonist. Thioperamide shows inverse agonism (enhances CAMP activity). The order of inhibitory activity of histamine derivatives was Histamine > N-alpha-methylhistamine > R(-)-alpha-methylhistamine > S(+)-alpha-methylhistamine. Both N-alpha-methylhistamine > R(-)-alpha-methylhistamine behave as full agonists.

CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.

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DR EMBL; AB044934; BAB13698.1; -

DR EMBL; AB045370; BAB20091.1; -

DR EMBL; AF307973; AAG32052.1; -

DR EMBL; AF312230; AAK12081.1; -

DR EMBL; AF329449; AAK43542.1; -

DR EMBL; AF325356; AAL01684.1; -

DR EMBL; AF298292; CAC83493.1; -

DR EMBL; AY136745; AAN01271.1; -

DR PIR; JC7566; JC7566.

DR Genew; HGNC:17383; HRH4.

DR MIM; 606792; -

DR GO; GO:0016021; C:integral to membrane; NAS.

DR GO; GO:0004969; F:histamine receptor activity; NAS.

DR InterPro; IPR000276; GPCR\_Rhodops.

DR InterPro; IPR008102; Histamrecept\_H4.

DR Pfam; PF00001; 7tm 1; 1.

DR PRINTS; PR00237; GPCRHHODOPS.

DR PRINTS; PR01726; HISTAMINEH4R.

DR PROSITE; PS00237; G-PROTEIN RECEPTOR FL1; 1.

DR PROSITE; PS00262; G-PROTEIN RECEPTOR FL2; 1.

KW G-protein coupled receptor; Glycoprotein; Lipoprotein; Palmitate; Transmembrane.

KW DOMAIN 1 19 Extracellular (Potential).

FT TRANSMEM 20 40 1 (Potential).

FT DOMAIN 41 52 Cytoplasmic (Potential).

FT TRANSMEM 53 73 2 (Potential).

FT DOMAIN 74 87 Extracellular (Potential).

FT TRANSMEM 88 108 3 (Potential).

FT DOMAIN 109 131 Cytoplasmic (Potential).

FT TRANSMEM 132 152 4 (Potential).

FT DOMAIN 153 172 Extracellular (Potential).

TRANSMBM 173 5 (Potential).  
FT DOMAIN 194 Cytoplasmic (Potential).  
FT DOMAIN 304 6 (Potential).  
FT TRANSMBM 305 Extracellular (Potential).  
FT DOMAIN 325 7 (Potential).  
FT TRANSMBM 342 7 (Potential).  
FT DOMAIN 362 7 (Potential).  
FT TRANSMBM 363 7 (Potential).  
FT DISULFID 87 By similarity.  
FT CARBOHYD 5 N-linked (GlcNAc...) (Potential).  
FT CARBOHYD 9 N-linked (GlcNAc...) (Potential).  
FT LIPID 374 8-palmitoyl cysteine (Potential).  
FT CONFLICT 138 A -> V (in Ref. 1).  
FT CONFLICT 206 H -> R (in Ref. 1).  
FT CONFLICT 253 Q -> R (in Ref. 1).  
SQ SEQUENCE 390 AA; 44495 MW; C986B8AE7FF912C3 CRC64;

Query Match 68.6%; Score 1403.5; DB 1; Length 390;  
Best Local Similarity 69.1%; Pred. No. 1.5e-95;  
Matches 271; Conservative 40; Mismatches 78; Indels 3; Gaps 2;

QY 1 MSESNGTDLPLTAQVPLAFMLSLAPAITGNNAVILAFVADRLRHRSNYFFLNLAIS 60  
Db 1 MPDTNSTNLSTRTVTAFFMNSLVAFALMGNALVILAFVVDKRLHRSNYFFLNLAIS 60  
QY 61 DFFVGVISIPIYPTLFTFEMDPKGCIVFWLTTDYLCTASVYIVLSYDRYQSVNAV 120  
Db 61 DFFVGVISIPIYPTLFTFEMDPKGCIVFWLTTDYLCTASVYIVLSYDRYQSVNAV 120  
QY 121 RYRAQHTGILKIVAOQVAVILAFVNGPMILASDWNKSTNTECEPGVTEWYILA 180  
Db 121 SYRTQHTGILKIVAOQVAVILAFVNGPMILASDWNKSTNTECEPGVTEWYILA 180  
QY 161 AFLEPLLVSVLVVYFVSVQIYVMSLWKGSIISRCPSHAGFIATSRGTGHSRRTGLACRTSL 240  
Db 179 SFLEFVIVPILVAYFNMNIYVMSLWKGSIISRCPSHAGFIATSRGTGHSRRTGLACRTSL 238  
QY 241 PGLKEPAASLHSES PRGKSSLLVSLRTHMSGSIIFKVGSCFRCSPVILHOREHVELL 300  
Db 239 SASTVPSFSPHSEPRGKSSLLVSLRTHMSGSIIFKVGSCFRCSPVILHOREHVELL 298  
QY 301 RKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYIAFWLQFNLSINPLFY 360  
Db 299 RRLAKSLAILLGVPAVCWAPYCLFTIVLSTYRGRPKSIWYIAFWLQFNLSINPLFY 358  
QY 361 PLCHRRFOKAFWKILCVTKQAPSPQ-TQSVSS 391  
Db 359 PLCHRRFOKAFWKILCVTKQAPSPQ-TQSVSS 390

RESULT 5  
Q8MNV9 PRELIMINARY; PRT; 390 AA.  
ID Q8MNV9  
AC Q8MNV9  
DT 01-MAR-2002 (TrEMBLrel. 20, Created)  
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine H4 receptor.  
OS Sus scrofa (Pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Cetartiodactyla; Suina; Suidae; Sus.  
OX NCBI\_TaxID=9823;  
RN [1]\_TaxID=9823;  
RP SEQUENCE FROM N.A.  
RC TISSUE=Spleen.  
RX MEDLINE=22015261; PubMed=12020829; DOI=10.1016/S0167-4781(02)00236-1;  
RA Oda T., Matsumoto S., Masuho Y., Takasaki J., Matsumoto M.,  
RA Kamohara M., Saito T., Onishi T., Soga T., Hiyama H., Matsushima H.,  
RA Furuichi K.,  
RT "cDNA cloning and characterization of porcine histamine H4 receptor";  
RL Biochim. Biophys. Acta 1575:135-138(2002).  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AB053300; BAB83078.1; -.  
GO; GO:0016021; C:integral to membrane; IEA.

DR GO:0004872; F:receptor activity; IEA.  
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHOOPS.  
DR PRINTS; PR01726; HISTAMINEH4.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.  
SQ SEQUENCE 390 AA; 44483 MW; BC8FD363A6F44D3F CRC64;

Query Match 65.0%; Score 1328.5; DB 2; Length 390;  
Best Local Similarity 66.9%; Pred. No. 5e-90;  
Matches 263; Conservative 29; Mismatches 96; Indels 5; Gaps 3;

QY 1 MSESNGTDLPLTAQVPLAFMLSLAPAITGNNAVILAFVADRLRHRSNYFFLNLA 58  
Db 1 MSAINDTNTPLNTRIALAFMLSLALVIMLGNVAVILAFVVDKRLHRSNYFFLNLA 60  
QY 59 ISDPFVGVISIPIYPTLFTFEMDPKGCIVFWLTTDYLCTASVYIVLSYDRYQSVNAV 118  
Db 61 ISDPFVGVISIPIYPTLFTFEMDPKGCIVFWLTTDYLCTASVYIVLSYDRYQSVNAV 120  
QY 119 AVYRAQHTGILKIVAOQVAVILAFVNGPMILASDWNKSTNTECEPGVTEWYILA 178  
Db 121 AVYRAQHTGILKIVAOQVAVILAFVNGPMILASDWNKSTNTECEPGVTEWYILA 178  
QY 179 ITAFLEPLLVSVLVVYFVSVQIYVMSLWKGSIISRCPSHAGFIATSRGTGHSRRTGLACRT 238  
Db 179 ITLFEPLAPVLLVAYFNMNIYVMSLWKGSIISRCPSHAGFIATSRGTGHSRRTGLACRT 238  
QY 239 SLPLKEPAASLHSES PRGKSSLLVSLRTHMSGSIIFKVGSCFRCSPVILHOREHVELL 298  
Db 239 SLSDPKAAASLHSES PRGKSSLLVSLRTHMSGSIIFKVGSCFRCSPVILHOREHVELL 297  
QY 299 RGRKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYIAFWLQFNLSINPLFY 358  
Db 298 RARKLARSLAVLSAFAICWAPYCLFTIVLSTYRGRPKSIWYIAFWLQFNLSINPLFY 357  
QY 359 LYPCHRRFOKAFWKILCVTKQAPSPQ-TQSVSS 391  
Db 358 LYPCHRRFOKAFWKILCVTKQAPSPQ-TQSVSS 390

RESULT 6  
Q912Y3 PRELIMINARY; PRT; 389 AA.  
ID Q912Y3  
AC Q912Y3  
DT 01-DEC-2001 (TrEMBLrel. 19, Created)  
DT 01-DEC-2001 (TrEMBLrel. 19, Last sequence update)  
DT 01-JUN-2003 (TrEMBLrel. 24, Last annotation update)  
DE Histamine H4 receptor.  
OS Cavia porcellus (Guinea pig).  
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
OC Mammalia; Eutheria; Rodentia; Hystricognathi; Caviidae; Cavia.  
OX NCBI\_TaxID=10141;  
RN [1]\_TaxID=10141;  
RP SEQUENCE FROM N.A.  
RA Liu C., Wilson S., Kuei C., Lovenberg T.W.;  
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.  
CC -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).  
CC -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.  
DR EMBL; AF358858; AAK97379.1; -.  
DR GO:0016021; C:integral to membrane; IEA.  
DR GO:0004872; F:receptor activity; IEA.  
DR GO:0001584; F:rhodopsin-like receptor activity; IEA.  
DR GO:0007186; F:G-protein coupled receptor protein signalin. .; IEA.  
DR Pfam; PF00001; 7tm\_1; 1.  
DR PRINTS; PR00237; GPCRHOOPS.  
DR PRINTS; PR01726; HISTAMINEH4.  
DR PROSITE; PS00237; G-PROTEIN RECEPTOR\_F1\_1; 1.  
DR PROSITE; PS00262; G-PROTEIN RECEPTOR\_F1\_2; 1.  
KW G-protein coupled receptor; Receptor; Transmembrane.



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or send an email to license@isb-sib.ch).
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EMBL; AF267537; AAF70947.1; --
EMBL; AF267538; AAF78950.1; --
DR InterPro; IPR000276; GPCR_Receptor.
DR Pfam; PF00001; 7tm_1_1;
DR PRINTS; PR00237; GPCR_HODOPSIN.
DR PRINTS; PR01471; HISTAMINE_H3R.
DR PROSITE; PS00337; G_PROTEIN_RECEPTOR_F1_1; 1.
DR PROSITE; PS0262; G_PROTEIN_RECEPTOR_F1_2; 1.
KW Alternative splicing; G-protein coupled receptor; Glycoprotein;
Transmembrane.
FT DOMAIN 1 40 Extracellular (Potential).
FT TRANSMEM 41 61 Potential.
FT DOMAIN 62 71 Cytoplasmic (Potential).
FT TRANSMEM 72 92 Potential.
FT DOMAIN 93 109 Extracellular (Potential).
FT TRANSMEM 110 130 Potential.
FT DOMAIN 131 157 Cytoplasmic (Potential).
FT TRANSMEM 158 178 Potential.
FT DOMAIN 179 197 Extracellular (Potential).
FT TRANSMEM 198 218 Potential.
FT DOMAIN 219 359 Cytoplasmic (Potential).
FT TRANSMEM 360 380 Potential.
FT DOMAIN 381 398 Extracellular (Potential).
FT TRANSMEM 399 419 Potential.
FT DOMAIN 420 445 Cytoplasmic (Potential).
FT DOMAIN 446 465 Poly-Ala.
FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).
FT VARSPIC 276 305 Missing (in isoform Short).
SQ SEQUENCE 445 AA; 48734 MW; BAE206A3887189A0 CRC64;
Query Match
Best Local Similarity 37.5%; Pred. No. 2.1e-43;
Matches 159; Conservative 54; Mismatches 132; Indels 79; Gaps 9;
QY 18 LAFLMSLAFAITGNVAVILAFVADRNLRHSNFFFLNLALSDFFVGVISPLIPIHTL 77
DB 38 LAALMALITVATVGLNVALVAFVADSSLRQTNFFLLNLALSDFLVGVFCIPLVPPYL 97
QY 78 F-NMPPGSGICMFLITDYLCTASVYSLVLSYDRYQSVNAVRYRAOHTGILKIVQM 136
DB 98 TORWTFGRGLCKMLVVDVLLCTSSVFNILVLSYDRFLSVTRAVSRAQGGQTRAVRNM 157
QY 137 VAVWTLAFVNGFMILASDNK-----NSTNTECEPGFVTEWYIILATFLEFLPVSL 191
DB 158 VLVWVLAFLLYGPAIL---SWEVLGGSSIPGHCVAEPFYNNWYFLITASTLEFFTPFLS 214
QY 192 VYFVSQIY-----WSLWKGKGSLSRCPSS 214
DB 215 VTFFNLSLYNTQRRTRLDGAREAGDPDLPPEAQSSPPQPPGCGWCPKGGESMPL 274
QY 215 HAGFTATSRG--TGHSRRRTGLACRTSLPGLKEPAASLHSESPRGKSSLLVSLRTHMSG 272
DB 275 HRYGVGEAGPAGAEALGGSGAAASTSSSGSSSRGTERPR----- 318
QY 273 IIAPKVGSFCRSESPVLHQ-----EHVLLRGRKLARSLLVLSAFAICWAPYCL 323
DB 319 --SLKRGSKPSASSASLEKRMKMWQSGITQRFRLSRDKKVAKSLAIVSIFGLCWAPYTL 376
QY 324 FTIVLSTVRRGRPKSIWYIAFWLQFNLSINPLYPICLHRRPQKAFKWLICVTK---Q 380
DB 377 LMIIRAAAC-HGHCVDPDYWYETSFVLLMANSVNPVLYPLCHYSFRRAFTKLLCPQKLKVQ 435
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QY 381 PAPS 384
DB 436 PHSS 439
RESULT 9
HH3R_HUMAN
ID HH3R_HUMAN STANDARD; PRT; 445 AA.
AC Q9Y5N1; Q9GZX2; Q9H4K8;
DT 28-FEB-2003 (Rel. 41, Created)
DT 28-FEB-2003 (Rel. 41, Last sequence update)
DE Histamine H3 receptor (HH3R) (G protein-coupled receptor 97).
GN Name=HRH3; Synonyms=GPCR97;
OS Homo sapiens (Human).
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN [1]_
RP SEQUENCE FROM N.A. (ISOFORM 1).
RC TISSUE=Thalamus;
RX MEDLINE=99278519; PubMed=10347254;
RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,
RA Huvar A., Jackson M.R., Erlander M.G.;
RT "Cloning and functional expression of the human histamine H3
RT receptor.";
RL Mol. Pharmacol. 55:1101-1107(1999).
RN [2]
RP SEQUENCE FROM N.A. (ISOFORM 2), AND CHARACTERIZATION.
RX MEDLINE=20568725; PubMed=1118334; DOI=10.1006/bbr.2000.4008;
RA Nakamura T., Itadani H., Hidaka Y., Ohta M., Tanaka K.;
RT "Molecular cloning and characterization of a new human histamine
RT receptor, HH4R.";
RL Biochem. Biophys. Res. Commun. 279:615-620(2000).
RN [3]
RP SEQUENCE FROM N.A. (ISOFORMS 1; 3; 4; 5; 6 AND 7).
RC TISSUE=Thalamus;
RX MEDLINE=21184713; PubMed=11284713; DOI=10.1042/0264-6021.3550279;
RA Coge F., Guenin S.-P., Audinot V., Renouard-Tray A., Beauverger P.;
RA Macia C., Ouvry C., Nagel N., Rique H., Boutin J.A., Galizzi J.P.;
RT "Genomic organization and characterization of splice variants of the
RT human histamine H3 receptor.";
RL Biochem. J. 355:279-288(2001).
RN [4]
RP SEQUENCE FROM N.A. (ISOFORM 1), AND VARIANT SHY-DRAGER SYNDROME
RP VAL-280.
RC TISSUE=Blood;
RX MEDLINE=21953383; PubMed=11956964; DOI=10.1007/s007020200036;
RA Wiedemann P., Boenisch H., Oerters F., Brues M.;
RT "Structure of the human histamine H3 receptor gene (HRH3) and
RT identification of naturally occurring variations.";
RL J. Neural Transm. 109:443-453(2002).
RN [5]
RP SEQUENCE FROM N.A. (ISOFORM 3).
RA Ullmer C., Zirwes E., Lubbert H.;
RT "Cloning and functional expression of the human histamine H3
RT receptor.";
RL Submitted (MAR-2001) to the EMBL/GenBank/DBJ databases.
RN [6]
RP SEQUENCE FROM N.A. (ISOFORM 1).
RX MEDLINE=21638749; PubMed=11780052; DOI=10.1038/414865a;
RA Deloukas P., Matthews L.H., Ashurat J.L., Burton J., Gilbert J.G.R.,
RA Jones M., Stavrides G., Almeida J.P., Babbage A.K., Bagguley C.L.,
RA Bailey J., Barlow K.F., Bates K.N., Beard L.M., Beare D.M.,
RA Beakley O.P., Bird C.P., Blakey S.E., Bridgeman A.M., Brown A.J.,
RA Buck D., Burrill W.D., Butler A.P., Carder C., Carter N.P.,
RA Chapman J.C., Clamp M., Clark G., Clark L.N., Clark S.Y., Clee C.M.,
RA Clegg S., Cobley V.E., Collier R.E., Connor R.E., Corby N.R.,
RA Coulson A., Coville G.J., Deadman R., Dhani P.D., Dunn M.,
RA Ellington A.G., Frankland J.A., Fraser A., French L., Garner P.,
RA Graham D.V., Griffiths C., Griffiths M.N.D., Gwilliam R., Hall R.E.,
RA Hammond S., Harley J.L., Heath P.D., Ho S., Holden J.L., Howden P.J.,
RA Huckle E., Hunt A.R., Hunt S.E., Jekosch K., Johnson C.M., Johnson D.,
```



QY 216 -----AGFIATSSRGTHSRRTGLACRTSLPGLKEPAASLHSPRGKSSLLV 263  
 DB 274 RYGVCEAAVGAEGATLGGGGGGS-----VASPTSSSG-----SSRGTERPR----- 318  
 QY 264 SLRTHMSGIIIAFKVSGPCRSFVLHQR-----EHVELLGRKLARSLAVLLSAP 314  
 DB 319 -----SLKRGSKPSASSASLEKRMKQVQSFTQRFRLSRDRKVAKSLAVIVSIF 367  
 QY 315 AICWAPYCLFIVLSTYRGRPKSIWYSIAPLWQFNLSLNPFLYPLCHRRFQKAFWKI 374  
 DB 368 GLCWAPYTLIIIRAAAC-HGHCVDPDYWYETSFLLWANSVNPVLPYLCHHSFRFAFTKL 426  
 QY 375 LCVTK---QPAPS 384  
 DB 427 LCPQKLKIQHSS 439

RESULT 10  
 HH3R MOUSE  
 ID HH3R MOUSE STANDARD; PRT; 445 AA.  
 AC P58406;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Histamine H3 receptor (HH3R).  
 GN Name=Hr3;  
 OS Mus musculus (Mouse).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.  
 OX NCBI\_TaxID=10090;  
 RN [1]  
 RP SEQUENCE FROM N.A.  
 RC STRAIN=CD-1;  
 RA Coge P., Rigue H., Levacher B., Leopold O., Guenin S.-P., Boutin J.A.,  
 RA Galizzi J.-P.;  
 RT Submitted (JUL-2001) to the EMBL/GenBank/DBJ databases.  
 RL "Cloning of mouse histamine H3 receptor";  
 CC -!- FUNCTION: The H3 subclass of histamine receptors could mediate the  
 CC histamine signals in CNS and peripheral nervous system. Signals  
 CC through the inhibition of adenylyl cyclase and displays high  
 CC constitutive activity (spontaneous activity in the absence of  
 CC agonist) (By similarity).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
 CC This SWISS-PROT entry is copyright. It is produced through a collaboration  
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 CC use by non-profit institutions as long as its content is in no way  
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 CC or send an email to [license@isb-sib.ch](mailto:license@isb-sib.ch)).  
 CC  
 CC EMBL; AY044153; AAK72406.1; -;  
 DR MGD; MGI:2139279; Hr3.  
 DR InterPro; IPR000276; GPCR Rhodopsin.  
 DR InterPro; IPR003980; H3\_receptor.  
 DR Pfam; PF00001; 7cwi; 1.  
 DR PRINTS; PR00237; GPCRHHODOPSN.  
 DR PRINTS; PR01471; HISTAMINEH3R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 39 Extracellular (Potential).  
 FT TRANSMEM 40 60 Potential.  
 FT DOMAIN 61 70 Cytoplasmic (Potential).  
 FT TRANSMEM 71 91 Potential.  
 FT DOMAIN 92 108 Extracellular (Potential).  
 FT TRANSMEM 109 129 Potential.  
 FT DOMAIN 130 156 Cytoplasmic (Potential).  
 FT TRANSMEM 157 177 Potential.  
 FT DOMAIN 178 196 Extracellular (Potential).  
 FT TRANSMEM 197 217 Potential.

FT DOMAIN 218 359 Cytoplasmic (Potential).  
 FT TRANSMEM 360 380 Potential.  
 FT DOMAIN 381 396 Extracellular (Potential).  
 FT TRANSMEM 397 417 Potential.  
 FT DOMAIN 418 445 Cytoplasmic (Potential).  
 FT DOMAIN 20 23 Poly-Ala.  
 FT CARBOHYD 11 11 N-linked (GlcNAc...) (Potential).  
 SQ SEQUENCE 445 AA; 48541 MW; B8D406E29E1F3C5F CRC64;  
 Query Match 33.5%; Score 686; DB 1; Length 445;  
 Best Local Similarity 37.1%; Pred. No. 1.5e-42;  
 Matches 159; Conservative 49; Mismatches 140; Indels 80; Gaps 10;

QY 18 LAFLMSLLAFPAITIGNAVILAFVADRLNRHSVFLNLAIISDPFGVVISIPLYPHTL 77  
 DB 37 LAALMALLIVATVIGNALVLAFAVADSLRTQNNFFLLNLAIISDELVAFCIPLVYPVL 96  
 QY 78 F-NMNPSSGICMFWLITDYLCTASVYSIVLISYDRYQSVSNVARYRAQHTGILKIVAQM 136  
 DB 97 TGRWTFGRGLCKLMLVVDYLLCASSVFNILISYDRPLSVTRAVSYRAQOGDTRRAVRKM 156  
 QY 137 VAVWILAFLVNGPMILASDSWK-----NSTWTECEPGFVTEWYILAITAFLEPLPVS 191  
 DB 157 ALVWLAFLYGPAIL-----SWEYLSGGSSIPGHCYAEFFYNWYFLITASTLEFPFLS 213  
 QY 192 VYFVSQIY-----WSLWKRGLSRCPSH 215  
 DB 214 VTFNLSIYLNIOQRTRLRLDGRAGPEPPDAPQPPPPPPGCGWPKHGEMPLH 273  
 QY 216 -----AG-FIATSSRGTHSRRTGLACR-----TSLPGLKEPAASLHSPRGKSSLL 262  
 DB 274 RYGVCEAGPGVETGEAGLGGGGGGAASPTSSSSSSSGTERPRSLKRGSKPSASSASL 333  
 QY 263 VSLRTHMSGIIIAFKVSGPCRSFVLHQRHVELLGRKLARSLAVLLSAPICWAPYC 322  
 DB 334 EKRMMVQSQI-----TQRFRLSRDKKVAKSLAIIVSIFGLCWAPYT 375  
 QY 333 LFTIVLSTYRGERPKSIWYSIAPLWQFNLSLNPFLYPLCHRRFQKAFWKILCVTK--- 379  
 DB 376 LLMIRAAC-HGHCVDPDYWYETSFLLWANSVNPVLPYLCHYSFRFAFTKLCPQKLKV 434  
 QY 380 QPAPSQTQ 387  
 DB 435 QPHGSLEQ 442

## RESULT 11

HH3R RAT  
 ID HH3R RAT STANDARD; PRT; 445 AA.  
 AC Q9QYN8; Q9QYN6; Q9QYN7; Q9QYN9;  
 DT 28-FEB-2003 (Rel. 41, Created)  
 DT 28-FEB-2003 (Rel. 41, Last sequence update)  
 DT 25-OCT-2004 (Rel. 45, Last annotation update)  
 DE Histamine H3 receptor (HH3R).  
 GN Name=Hr3;  
 OS Rattus norvegicus (Rat).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Rattus.  
 OX NCBI\_TaxID=10116;  
 RN [1]  
 RP SEQUENCE FROM N.A. (ISOFORM 1).  
 RC TISSUE=Hypothalamus;  
 RX MEDLINE=20330707; PubMed=10869375;  
 RA Lovenberg T.W., Pyati J., Chang H., Wilson S.J., Brlander M.G.;  
 RT "Cloning of rat histamine H3 receptor reveals distinct species  
 RT pharmacological profiles";  
 RL J. Pharmacol. Exp. Ther. 293:771-778 (2000).  
 RN [2]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1 AND 2).  
 RC TISSUE=Striatum;  
 RX MEDLINE=21016732; PubMed=11130725; DOI=10.1038/35048583;  
 RA Morisset S., Rouleau A., Ligneau X., Gbahou F., Tardivel-Lacombe J.,  
 RA Stark H., Schunack W., Ganelin C.R., Schwartz J.-C., Arrang J.-M.;

RT "High constitutive activity of native H3 receptors regulates histamine neurons in brain.";  
 RL Nature 408:860-864 (2000).  
 RN [3]  
 RP SEQUENCE FROM N.A. (ISOFORMS 1; 2; 3 AND 4).  
 RA Itadani H., Takimura T., Nakamura T., Ohta M.;  
 RT "Cloning of a novel G protein-coupled receptor.";  
 RL Submitted (JUN-1998) to the EMBL/GenBank/DBJ databases.  
 RN [4]  
 RP TISSUE SPECIFICITY.  
 RX MEDLINE=99278519; PubMed=10347254;  
 RA Lovenberg T.W., Roland B.L., Wilson S.J., Jiang X., Pyati J.,  
 RA Huvar A., Jackson M.R., Briander M.G.;  
 RT "Cloning and functional expression of the human histamine H3 receptor.";  
 RL Mol. Pharmacol. 55:1101-1107 (1999).  
 CC -!- FUNCTION: The H3 subclasses of histamine receptors could mediate the histamine signals in CNS and peripheral nervous system. Signals through the inhibition of adenylyate cyclase and displays high constitutive activity (spontaneous activity in the absence of agonist).  
 CC -!- SUBCELLULAR LOCATION: Integral membrane protein.  
 CC -!- ALTERNATIVE PRODUCTS:  
 CC Event=Alternative splicing; Named isoforms=4;  
 CC Comment=Additional isoforms seem to exist;  
 CC Name=1; Synonyms=H3L;  
 CC IsoId=Q9QYN8-1; Sequences=Displayed;  
 CC Name=2; Synonyms=H3S;  
 CC IsoId=Q9QYN8-2; Sequences=VSP\_001887;  
 CC Name=3;  
 CC IsoId=Q9QYN8-3; Sequences=VSP\_001888;  
 CC Name=4;  
 CC IsoId=Q9QYN8-4; Sequences=VSP\_001889;  
 CC -!- TISSUE SPECIFICITY: Expressed abundantly in brain, most notably throughout the thalamus, the ventromedial hypothalamus and the caudate nucleus. Isoform 1 is largely predominant in all tissues.  
 CC -!- MISCELLANEOUS: Proxifan acts as a potent neutral antagonist while thaloproamide, ciproxifan and FUB465 act as potent inverse agonists.  
 CC -!- SIMILARITY: Belongs to the G-protein coupled receptor 1 family.  
 CC  
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 CC  
 DR EMBL; AF237919; AAF82086.1; -;  
 DR EMBL; AY009370; AAK02069.1; -;  
 DR EMBL; AB015646; BAA88765.1; -;  
 DR EMBL; AB015646; BAA88766.1; -;  
 DR EMBL; AB015646; BAA88767.1; -;  
 DR EMBL; AB015646; BAA88768.1; -;  
 DR RGD; 620630; Hrh3.  
 DR InterPro; IPR000276; GPCR\_Rhodpsn.  
 DR InterPro; IPR003980; H3\_receptor.  
 DR Pfam; PF00001; 7tm\_1; 1\_  
 DR PRINTS; PR00237; GPCRHOOPS.  
 DR PRINTS; PR01471; HISTAMINEH3R.  
 DR PROSITE; PS00237; G\_PROTEIN\_RECEP\_F1\_1; 1.  
 DR PROSITE; PS0262; G\_PROTEIN\_RECEP\_F1\_2; 1.  
 KW Alternative splicing; G-protein coupled receptor; Glycoprotein; Transmembrane.  
 FT DOMAIN 1 39 Extracellular (Potential).  
 FT TRANSMEM 40 60 Potential.  
 FT DOMAIN 61 70 Cytoplasmic (Potential).  
 FT TRANSMEM 71 91 Potential.  
 FT DOMAIN 92 108 Extracellular (Potential).  
 FT TRANSMEM 109 129 Potential.  
 FT DOMAIN 130 156 Cytoplasmic (Potential).  
 FT TRANSMEM 157 177 Potential.

FT DOMAIN 178 196 Extracellular (Potential).  
 FT TRANSMEM 197 217 Potential.  
 FT DOMAIN 218 359 Cytoplasmic (Potential).  
 FT TRANSMEM 360 380 Potential.  
 FT DOMAIN 381 396 Extracellular (Potential).  
 FT TRANSMEM 397 417 Potential.  
 FT DOMAIN 418 445 Cytoplasmic (Potential).  
 FT DOMAIN 20 23 Poly-Ala.  
 FT CARBOHYD 11 11 Missing (in isoform 2).  
 FT VARSPLIC 274 305 /FTId=VSP\_001887.  
 FT VARSPLIC 274 321 Missing (in isoform 3 and isoform 4).  
 FT VARSPLIC 393 445 /FTId=VSP\_001888.  
 FT VARSPLIC 393 445 WYETFWLWNSAVNPVLYPLCHVSFRAPTKLLCPQKLUK VQHGSLQEWK -> CVERLGLKEASLLPLLMFSGRRR LKAVCELDVPMFNOERQNCRCGARGWIGRCGLPRPPSVLQ RPAEPROLLPAPPGCLGRWPCPCPCVCTIRIWGWVMG (in isoform 4).  
 FT /FTId=VSP\_001889.  
 SQ SEQUENCE 445 AA; 48588 MW; 63DFEFC21758F5B CRC64;  
 Query Match 33.3%; Score 682; DB 1; Length 445;  
 Best Local Similarity 37.0%; Pred. No. 2.9e-42;  
 Matches 160; Conservative 51; Mismatches 133; Indels 88; Gaps 10;  
 QY 18 LAFLMSLLAFATIGNAVVILAFVADRNLRHSNFFFLNLASDFVGVISIPLYIPHTL 77  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 37 LAALMALLIVATVLGNALVLAFAVDSSLRQNNFLLNLASDFLVGAFCLPLYVPYVL 96  
 QY 78 F-NNPFGSICMFMLITDYLLCTASVYSIVLISYDYQSVSNVRYRAQHTGLKIVAQ 136  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 97 TGRWTFGRGLCKLWLVVDYLLCASSVFNIVLISYDFLVSFVRAVYRAQGGDTRRAVRKM 156  
 QY 137 VAVWILAFVNGPMILASDSWK-----NSTNTECEPGEVTEWYILAITAFLEFLPVSL 191  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 157 ALVWVLAFLLYGPAIL---SWEYLSGGSSIPGCHYAEFFYNWYFLITASTLEFFTPFLS 213  
 QY 192 VYVFSVQIY-----WMLWKRGSLSRCPSH 215  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 214 VTFFNLSTYLNQRTLRLLDGRAGPEPPDAPSPPPAPPCWGCWPKHGHEAMPLH 273  
 QY 216 AGFIATSSRG-----GHSRRTGLACTSLPLGLKEPAASLHSESPRKSSLLVSLRT 267  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 274 RYGVGEAGPGVBAALGGSGGGAASPTSSG-----SSSRGTERPR----- 318  
 QY 268 HMSGSIIFKVGSCFCSFVLHQR-----EHVELLRGKRLARSLAVLLSAFAICW 318  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 319 -----SLKRGSKPSASSASLEKMKVVSQSIQTFRLSRDKKVAKSLAIIVIFGLCW 371  
 QY 319 APYCLFTIVLSTYRRGERPKSIWYIAFWLQFNLSINPFLYPLCHRRFQKAPWKILCVT 378  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 372 APYLLMIIRAAC-HGRCPIDYWYETSFLLWANGAVNPVLYPLCHYSFRRAFTKLLCPQ 430  
 QY 379 K---OPAPSQTQ 387  
 DB |||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|||||:|  
 431 KLKVPQPHGSLEQ 442  
 RESULT 12  
 Q6ZM33  
 ID Q6ZM33 PRELIMINARY; PRT; 473 AA.  
 AC Q6ZM33;  
 DT 05-JUL-2004 (TReMBLrel. 27, Created)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last sequence update)  
 DT 05-JUL-2004 (TReMBLrel. 27, Last annotation update)  
 DE SI:bz34g2.4 (Novel protein similar to human histamine receptor H3 (HRH3)).  
 DE Name=si:rp71-34g2.4; Synonyms=SI:bz34g2.4;  
 OS Brachydanio rerio (Zebrafish) (Danio rerio).  
 OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;  
 OC Actinopterygii; Neopterygii; Teleostei; Ostariophysi; Cypriniformes;  
 OC Cyprinidae; Danio.  
 OX NCBI\_TaxId=7955;

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RN  [1]
RP  SEQUENCE FROM N.A.
RA  Tracey A.;
RL  Submitted (OCT-2003) to the EMBL/GenBank/DBJ databases.
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC  -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR  EMBL; AL928906; CAE49238.1; -.
DR  ZFIN; ZDB-GENE-040724-204; si:rp71-34g2.4.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004872; F:histamine receptor activity; IEA.
DR  GO; GO:0004969; F:histamine receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; F:rhodopsin-like receptor activity; IEA.
DR  InterPro; IPR000276; GPCR_Rhodopsin.
DR  InterPro; IPR003980; H3_receptor.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRRHODOPSIN.
DR  PRINTS; PR01471; HISTAMINEH3R.
DR  PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW  G-protein coupled receptor; Receptor; Transmembrane.
SQ  SEQUENCE 473 AA; 53506 MW; 032FC7C27D8C6E57 CRC64;

Query Match      32.8%; Score 671; DB 2; Length 473;
Best Local Similarity 38.1%; Pred. No. 2e-41;
Matches 169; Conservative 60; Mismatches 143; Indels 72; Gaps 15;

QY  1 MSEGNTDVLPL-----TAQVPLAFMLSLAFATIGNAVVILAFVADRN 45
DB  35 MERNATSLADLTDPENRAQYGFSPSTSLFTVLTMTLLVPATVLGNALVILAFVWEKS 94
QY  46 LRHSNYEFLNLATSDFPVGVISPLYPHTLP-NWNPSSGICMPMLITDYLCTASVYS 104
DB  95 LRTQNFPLNLATADFLVGGFCIPVLYLTGEWRLGRGCKLWLVVDMLCTASVFN 154
QY  105 IVLISYDRYQSVNAVRYRAQHTGLK-IVAQMVAWITLAFVNGPMLIASDSKNSTNT 163
DB  155 IVLISDFDRFQSVTKAVSYRCQ-KGITKDAVLKMLCVLAAPFLYGPAIL---SWEHTGG 210
QY  164 E-----ECEPFVTEWYILATAFLEFLPLVSLVYPSVQIYWSLWKR----- 206
DB  211 SVVPDGECAEFYFNWYFLMTASTVEFTPTFISVTYFNLSIYINRNRCAMREEQTYVR 270
QY  207 -GSLRCPSHAG-----FIATSSRGHSGHRTGLACRTSLPGL-----KEPAASLHS--E 253
DB  271 LRSFKMKPLGADVQRVEFV----RPVEESRVADLASRCCRLASTAKVSAAPFGNGRQ 326
QY  254 SPRGKSSLLVSLRTHMSGSIIAFKVGSF---CRSESPLYHQEHV-----ELLRGRKL 303
DB  327 SKRRDSTLADLPPLQVEERILAASEAQPHYVDHSAGPHRRPDMVASLANRFLSRDKKV 386
QY  304 ARSLAVLSAFAICWAPCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLNPFLYPLC 363
DB  387 AKSLAVIVCVFGLCWAPYLLMIIRAAC-HGQCQVQHYLYEISFWLLWINSINPILYPLC 445
QY  364 HRRFOKAFWKILCVTKQAPASQTQ 387
DB  446 HSRFKRFSKLLC-----PSKTK 463
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RESULT 13
Q8WY01 PRELIMINARY; PRT; 365 AA.
AC Q8WY01
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Histamine H3 receptor isoform 2.
GN Name=HRH3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
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RN  [1]
RP  SEQUENCE FROM N.A.
RA  TISSUE-Hippocampus;
RA  Wellendorph P.; Goodman M.W.; Burstein E.S.; Nash N.R.; Brann M.R.;
RA  Weiner D.M.;
RT  "Molecular Cloning and Characterization of Functionally Distinct
RT  Isoforms of the Human Histamine H3 Receptor.";
RL  Neuropharmacology 0:0-0(2002)
CC  -1- SUBCELLULAR LOCATION: Integral membrane protein (By similarity).
CC  -1- SIMILARITY: Belongs to family 1 of G-protein coupled receptors.
DR  EMBL; AF321911; AAL71912.1; -.
DR  GO; GO:0016021; C:integral to membrane; IEA.
DR  GO; GO:0004969; F:histamine receptor activity; IEA.
DR  GO; GO:0004872; F:receptor activity; IEA.
DR  GO; GO:0001584; F:rhodopsin-like receptor activity; IEA.
DR  GO; GO:0007186; F:rhodopsin-like receptor activity; IEA.
DR  Pfam; PF00001; 7tm_1; 1.
DR  PRINTS; PR00237; GPCRRHODOPSIN.
DR  PRINTS; PR01471; HISTAMINEH3R.
DR  PROSITE; PS00237; G_PROTEIN_RECP_F1_1; 1.
DR  PROSITE; PS0262; G_PROTEIN_RECP_F1_2; 1.
KW  G-protein coupled receptor; Receptor; Transmembrane.
SQ  SEQUENCE 365 AA; 40609 MW; D78B32042464CB35 CRC64;

Query Match      32.2%; Score 658; DB 2; Length 365;
Best Local Similarity 39.0%; Pred. No. 1.4e-40;
Matches 152; Conservative 44; Mismatches 104; Indels 90; Gaps 11;

QY  18 LAFMLSLAFATIGNAVVILAFVADRNLRHSNYEFLNLATSDFPVGVISPLYPHTL 77
DB  37 LAALMALLIVATVLGNALVILAFVADSSLRQTQNNFFLLNLATSDPLVGAFCLPYVPYL 96
QY  78 P-NWNPSSGICMPMLITDYLCTASVYSIVLISVDVRSVNAVRYRAQHTGLKIVAQM 136
DB  97 TGRWTFGRGLCKLWLVVDYLLCTSSAFNVLISVDRFLSVTRAVSYRAQQGQDTRAVRKM 156
QY  137 VAVVILAFVNGPMLIASDSWK-----NSTNTECEPGFVTEWYILATAFLEFLPLVSL 191
DB  157 LLVWVLAFLYGPAIL---SWEYLSGGSSIPEGHCHYAEFFYNWYFLITASTLEFFTPFLS 213
QY  192 VYFVSQIYWSLWKRGLSRCPSHAGFTATSSRGHSGHRTGLACRTSLPGLKE----- 245
DB  214 VTFFNLISYILNI-----QRRT-----RLRDGAREAAAGPEP 244
QY  246 -PAASLHSESPRGKSSLLVSLRTHMSGSIIAFKVGSFC-----RSESPLYHQEHVEL 297
DB  245 PFEAQSPSPPPPG-----CWGCWQKHGGEAMPLH----- 273
QY  298 LRGRKLARSLLAVLSAFAICWAPCLFTIVLSTYRRGERPKSIWYSIAFWLQWNSLNP 357
DB  274 --RKVAKSLAVIVSIFGLCWAPYLLMIIRAAC-HGCHVDYDWTYSFLLWANSVNP 329
QY  358 FLYPLCHRRFPQAFWKILCVTK---QPAPS 384
DB  330 VLYPLCHHSFRRAFTKLLCPQLKIQPHSS 359

RESULT 14
Q8WXX29 PRELIMINARY; PRT; 373 AA.
AC Q8WXX29
DT 01-MAR-2002 (TrEMBLrel. 20, Created)
DT 01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
DE Histamine H3 receptor isoform 4.
GN Name=HRH3;
OS Homo sapiens (Human);
OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
OC Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
OX NCBI_TaxID=9606;
RN  [1]
RP  SEQUENCE FROM N.A.
RA  TISSUE-Hippocampus;
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